



Sequence Listing

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Botstein, David
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Eaton, Dan
Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljasin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.

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Trp Trp Pro Leu Ala Leu Ile Leu Ala Thr Gln Arg Ile Ser Arg	245	250	255
Pro Ile Val Asn Leu Phe Val Ser Arg Asp Leu Gly Gly Ser Ser	260	265	270
Ala Ala Thr Glu Ala Val Ala Ile Leu Thr Ala Thr Tyr Pro Val	275	280	285
Gly His Met Pro Tyr Gly Trp Leu Thr Glu Ile Arg Ala Val Tyr	290	295	300
Pro Ala Phe Asp Lys Asn Asn Pro Ser Asn Lys Leu Val Ser Thr	305	310	315
Ser Asn Thr Val Thr Ala Ala His Ile Lys Lys Phe Thr Phe Val	320	325	330
Cys Met Ala Leu Ser Leu Thr Leu Cys Phe Val Met Phe Trp Thr	335	340	345
Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Met Gly Leu Ser Thr Phe Thr Ala Ile Ala Ala Gly Thr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8
<211> 535
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 33, 66, 96, 387
<223> unknown base

<400> 8
ctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50
tgagttcttg gtgscntttg gctctaattc tggccacaca gagaancagt 100
cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150
agccacagag gcagtggcga ttttgacagc cacataacct gtgggtcaca 200
tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250
agaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300
gccccacatc aagaagttca ccttcgtctg catggctctg tcaclacgc 350
ttgttttctg gatgttttgg acaccccaag tgcctgngaa atctttgata 400
gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccctt 450
gggatcttcc tctttcttcc cagttccagt cacagtgagg ggcacatcca 500
ccgggtggct gatgacactg aagaaaacct tcgtc 535

<210> 9
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273,
293, 296, 305, 336, 358, 361
<223> unknown base

<400> 9
tggaggaata caggataga tttcttgtt tggaggaat cccccccac 50
cctcctctg ggaatcttt ccccccttc cccccccac cccccccac 100
agttcaacct gtttgnata gntctgtcaa ctccagctnt atttctaat 150
gttttgaca cccaaagtat ttgaqaaat tttgatagac atnatcggag 200
tggantttgc ctttgacaaa ntttgnngtg ttcttttgcg gattttctcc 250
tttttccag ttccagtcac agnqagaaa catctcacc ggngantat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350
ttgtcctnat ngccagcctt gtggctctac cctacctggg ggtgcacggg 400
gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 14
ccttcgcgcca cggagttc 18

<210> 15
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 15
ggcaaagtcc actccgatga tgtc 24

<210> 16
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 16
gactgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
ctagggagca ggccttgacc cggggatctg agtctgtaca ggagg 47

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
cctcccgagcc cggcgccggg cgcctgaagg cgggacccac cgcctatggg 50
gactgactgg gagcctgtct cctgtccagc tgcgcgtcct gcctctggg 100
ctctgacccc tgcctctgtg agactgtgtg ccccgccagc cgcgaactca 150

cogtgagcgc cctcatcttc acgtttcttc tcttctggg ggtgctggtg 200
tccatcatta tgetgagccc gggcgtggaq agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg ccgggatccc caccgtcttg cagggccaca 300
tcgactgtgg ctccctgett ggcacccgcg ctgtctaccg catgtgcttc 350
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gagcagcagc cgggaccccc gggtgccat ccagaatggg ttttggttct 450
ttaagtctct gatcctggtg ggctccaccg tgggtgcctt ctacatccct 500
gacggctcct tcaccaacat ctggttctac ttccggctcg tgggtcctt 550
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tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700
ggcgtggcg ctgatgttca tgtactaac tgagccagc ggctgccacg 750
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gctgcaggcc tcggtcatca cctctaacac catgtttgtc acctggtcag 900
ccctatccag tatcctgaa cagaaatgca accccattt gccaacccag 950
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cagaccgagg agtgccacc tatgttagac gccacacagc agbagcagca 1150
gcaggtggca gctgtgagg gccgggcctt tgacaacgag caggacggcg 1200
tcacctacag ctactcttc ttccactctt gctcgtctgt ggcctcactg 1250
cagtcctga tgaggtcac caactggtac aacccagtg agaccccaa 1300
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gcagctggg 1350
cagggtgct cctctacctg tggacctgg tagcccaact cctcctgcgc 1400
aacccgact tcagctgagg cagcctaca gctgcctc tggtgccctc 1450
tgccacctgg tgctctcgg ctcggtgaca gccaacctgc cccctccca 1500
caccaatcag ccagctgag ccccaacccc tgcccagct ccaggacctg 1550
ccctgagcc gggccttata gtctagtgc ctccagggtc ccaggagcat 1600

caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650
 cctcttcctt cccctctccc ctgttgccca tactcagcat ctcgatgaa 1700
 agggctccct tgtctcagg ctccaaggga gcggggctgc tggagagagc 1750
 ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800
 tggtcacgtc cccagggga cctgcccccc ttctggact tegtgcctta 1850
 ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900
 a 1901

<210> 19
 <211> 457
 <212> PRT
 <213> Homo sapiens

<400> 19
 Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser
 1 5 10 15
 Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro
 20 25 30
 Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe
 35 40 45
 Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly
 50 55 60
 Val Glu Ser Gln Leu Tyr Lys Leu Pro Trp Val Cys Glu Glu Gly
 65 70 75
 Ala Gly Ile Pro Thr Val Leu Gln Gly His Ile Asp Cys Gly Ser
 80 85 90
 Leu Leu Gly Tyr Arg Ala Val Tyr Arg Met Cys Phe Ala Thr Ala
 95 100 105
 Ala Phe Phe Phe Phe Phe Thr Leu Leu Met Leu Cys Val Ser
 110 115 120
 Ser Ser Arg Asn Ile Arg Asn Asn Ser Val Asn Tyr Ile Trp Phe
 125 130 135
 Phe Lys Phe Leu Ile Leu Val Gly Leu Thr Val Gly Ala Phe Tyr
 140 145 150
 Ile Pro Asp Gly Ser Phe Thr Asn Ile Trp Phe Tyr Phe Gly Val
 155 160 165
 Val Gly Ser Phe Leu Phe Ile Leu Ile Gln Leu Val Leu Leu Ile
 170 175 180

Asp Phe Ala His Ser Trp Asn Gln Arg Trp Leu Gly Lys Ala Glu
185 190 195

Glu Cys Asp Ser Arg Ala Trp Tyr Ala Gly Leu Phe Phe Phe Thr
200 205 210

Leu Leu Phe Tyr Leu Leu Ser Ile Ala Ala Val Ala Leu Met Phe
215 220 225

Met Tyr Tyr Thr Glu Pro Ser Gly Cys His Glu Gly Lys Val Phe
230 235 240

Ile Ser Leu Asn Leu Thr Phe Cys Val Cys Val Ser Ile Ala Ala
245 250 255

Val Leu Pro Lys Val Gln Asp Ala Gln Pro Asn Ser Gly Leu Leu
260 265 270

Gln Ala Ser Val Ile Thr Leu Tyr Thr Met Phe Val Thr Trp Ser
275 280 285

Ala Leu Ser Ser Ile Pro Glu Gln Lys Cys Asn Pro His Leu Pro
290 295 300

Thr Gln Leu Gly Asn Glu Thr Val Val Ala Gly Pro Glu Gly Tyr
305 310 315

Glu Thr Gln Trp Trp Asp Ala Pro Ser Ile Val Gly Leu Ile Ile
320 325 330

Phe Leu Leu Cys Thr Leu Phe Ile Ser Leu Arg Ser Ser Asp His
335 340 345

Arg Gln Val Asn Ser Leu Met Gln Thr Glu Glu Cys Pro Pro Met
350 355 360

Leu Asp Ala Thr Gln Gln Gln Gln Gln Gln Val Ala Ala Cys Glu
365 370 375

Gly Arg Ala Phe Asp Asn Glu Gln Asp Gly Val Thr Tyr Ser Tyr
380 385 390

Ser Phe Phe His Phe Cys Leu Val Leu Ala Ser Leu His Val Met
395 400 405

Met Tyr Leu Thr Asn Trp Tyr Arg Ser Gly Thr Thr Ala Lys Met
410 415 420

Ile Ser Thr Trp Thr Ala Val Trp Val Lys Ile Cys Ala Ser Trp
425 430 435

Ala Gly Leu Leu Leu Tyr Leu Trp Thr Leu Val Ala Pro Leu Leu
440 445 450

Leu Arg Asn Arg Asp Phe Ser
455

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 20
gccgctcat cttcacgttc ttcc 24

<210> 21
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 21
tcattccagct ggtgctgctc 20

<210> 22
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 22
ctttcttcac ttctgcttgg 20

<210> 23
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 23
cttgggcaaaa aatgcaac 18

<210> 24
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 24
caggaatgta gaaggcacc acgg 24

<210> 25
<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 25
tggcacagat cttcacccac acgg 24

<210> 26
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 26
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27
<211> 1351
<212> DNA
<213> Homo sapiens

<400> 27
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50
ttaacctggg tcaaatgcac ggattctcac ctctacagt tacgctctcc 100
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgctcgt 150
aggctcgagag aaggccatgg aggtgccgcg accggcaccg cggagctttc 200
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250
actgcgcgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300
cccagagccc tattaccgag aatctggatg ggaccgcctc cgggagctgt 350
ttggcaaaga tgaacagcag agaatttcaa aggacottgc taatatctgt 400
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450
agcttttatt catctctaac aacaatacat tgagcagagc caggcagaaa 500
tttatcataa ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550
cgaggcttca ttcttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600
tgtgactata ttcaacacag tgaacaactag tctgaatgta taccgaaata 650
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700
tttaggataa acgtaggcct gcgtggcctg gtggctgggt gcataattgg 750
agccttgctg ggcactcctg taggaggcct gctgatggca ttccagaagt 800

acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850
catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900
cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950
atgctaagaa aattgaagca ctgctaaacc ttctagaaa cccttcagta 1000
atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050
gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100
tctttggtea gctgtctgac aaatttaagt gctggtagct gtggtggcag 1150
tggttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200
gtactctcac ttacttata cttaaattta aatacatact tatgtttgta 1250
ttaatctata aatatatgca tacatggata tatccacca cctagatttt 1300
aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350
t. 1351

<210> 28
<211> 285
<212> PRT
<213> Homo sapiens

<400> 28
Met Glu Val Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala
1 5 10 15
Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala
20 25 30
Asp Ser Glu Val Leu Glu Glu Arg Gln Lys Arg Leu Pro Tyr Val
35 40 45
Pro Glu Pro Tyr Tyr Pro Glu Ser Gly Trp Asp Arg Leu Arg Glu
50 55 60
Leu Phe Gly Lys Asp Glu Gln Gln Arg Ile Ser Lys Asp Leu Ala
65 70 75
Asn Ile Cys Lys Thr Ala Ala Thr Ala Gly Ile Ile Gly Trp Val
80 85 90
Tyr Gly Gly Ile Pro Ala Phe Ile His Ala Lys Gln Gln Tyr Ile
95 100 105
Glu Gln Ser Gln Ala Glu Ile Tyr His Asn Arg Phe Asp Ala Val
110 115 120
Gln Ser Ala His Arg Ala Ala Thr Arg Gly Phe Ile Arg Tyr Gly
125 130 135

Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	
				140					145					150	
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	
				155					160					165	
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	
				170					175					180	
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	
				185					190					195	
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	
				200					205					210	
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	
				215					220					225	
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	
				230					235					240	
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	
				245					250					255	
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	
				260					265					270	
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	
				275					280					285	

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 24

cggaagtcgc ttgaggagcg tcagaagcgg ctccctacg tccagagcc 50

ctattacccg gaatctggat gggaccgctc cgaggagctgt ttggcaaaga 100

tgaacagcag agaatttcaa aggacottgc taatatctgt aagacggcag 150

ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200

catggttacc aatacaacat tggagctggtg caggcagaa ttatctctaa 250

tgggttggat gctgtggaat ctgcacatca tctgcaaaa cggagcttca 300

ttcgtttatg gctggcgcag aacc 324

<210> 30

<211> 377

<212> DNA

<213> Homo sapiens

<220>

<221> unsure
<222> 262, 330, 371
<223> unknown base

<400> 30
tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccggc 50

accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100
gctgccgaag ctgtgactgc cgattcggaa gtcottgagg agcgtcagaa 150
gcggttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200
gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250
cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300
gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350

agagccaggc agaaatttat nataacc 377

<210> 31
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 31
tcgtacagtt acgctctccc 20

<210> 32
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
cttgaggagc gtcagaagcg 20

<210> 33
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 33
ataacgaatg aagcctcgtg 20

<210> 34
<211> 40
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 34

gctaatatct gtaagacggc agctacagca ggcatcattg 40

<210> 35

<211> 1819

<212> DNA

<213> Homo sapiens

<400> 35

gagccgccgc cgcgcgcgcg ccgcgcactg cagccccagg ccccgccccc 50
ccacccacgt ctgcgttgct gcccgcctg ggccaggccc caaaggcaag 100
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150
tgccggcaac cacaggttcc aagatggttt gcgggggctt cgcgtgttcc 200
aagaactgcc tgtgcgcctt caacctgctt tacaccttgg ttagtctgct 250
gctaattqga attgctgctt ggggcattgg ctccgggctg atttccagtc 300
tccgagtggc cggcgtggtc attgcagtgg gcattctctt gttcctgatt 350
gcttttagtgg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400
tttttatatg attattctgt tacttgtatt tattgttcag tttctgtat 450
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500
gttggttggg acaatacggc aagtgtctga aatgacatcc agagaaatct 550
aaactgctgt gggttccgaa gtgttaaccc aaatgacacc tgtctggcta 600
gctgtgttaa aagtgaccac tcgtgtctgc catgtgtctc aatcatagga 650
gaatatgctg gagaggtttt gagatttgtt ggtggcattg gctgtttctt 700
cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750
agaaaagacc ccgcgcgaat cctagtgcct tcttttgatg agaaaacaag 800
gaagatttcc ttctgtatta tgatcttgtt caatttctgt aattttctgt 850
taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900
ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950
ttttctttcc gttgctgaaa aatatttgaa acttgtggtc tctgaagctc 1000
gttggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050
cctttcttag cttttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100

ttggttatat ggtgaatctg aacgtacatc tcaactgggtat aattatatgt 1150
 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200
 taaaatcaga aagtatgaga tctgttatg ttaagggaaa tccaaattcc 1250
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450
 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550
 aagactgcat ttttaaacia gttagtatta atgcgttggc ccacgtagca 1600
 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcatgaaat 1650
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttqaatatg 1700
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tglatatctt 1750
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800
 taaaagaaag taatggaag 1819

<210> 36
 <211> 204
 <212> PRT
 <213> Homo sapiens

<400> 36
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala
 1 5 10 15
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile
 20 25 30
 Ala Ala Trp Gly Ile Gly Phe Gly Leu Ile Ser Ser Leu Arg Val
 35 40 45
 Val Gly Val Val Ile Ala Val Gly Ile Phe Leu Phe Leu Ile Ala
 50 55 60
 Leu Val Gly Leu Ile Gly Ala Val Lys His His Gln Val Leu Leu
 65 70 75
 Phe Phe Tyr Met Ile Ile Leu Leu Leu Val Phe Ile Val Gln Phe
 80 85 90
 Ser Val Ser Cys Ala Cys Leu Ala Leu Asn Gln Gln Gln Gln Gly
 95 100 105

<223> unknown base

<400> 38

aatcccaaat tccccaattt ttttggnctt tttagggaaa gatgtgttgt 50
ggtaaaaaagt gttagtataa aaatgataat ttacttgtag tcttttatga 100
ttacaccaat gtattctaga atagttatgt cttaggaaat tgtgggttaa 150
tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200
tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250
ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300
taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgog 350
ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400
ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450
gcataattga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500
ggaggaaatg gcaatcttat gtgtgtctga ggacacagta agagcaccaa 550
gttgtgcccc acttgc 566

<210> 39

<211> 264

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 84-85, 206

<223> unknown base

<400> 39

atgattatc tgttacttgt atttattgtt cagttttatg gtatcttgcg 50
cttttttagc ccttgaacc aggagcaaca gggncagct ccttggaggt 100
tgtttggcaa caatcacggc caagtgactc cgcaaatac atcccagaga 150
aatcttaaac tgtgtgggtt tccgaagtgt taactcaaat gacactgtc 200
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<223> Synthetic oligonucleotide probe

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<220>
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<400> 41
gaqaatatgc tggagagg 18

<210> 42
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<220>
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<400> 42
tqqaatgcac taqqattcgc gcgc 24

<210> 43
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<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 43
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<210> 44
<211> 2061
<212> DNA
<213> Homo sapiens

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<210> 45
 <211> 359
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe
 50 55 60
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val
 65 70 75
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe
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 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp
 95 100 105
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly
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 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys
 125 130 135
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro
 140 145 150
 Gly Pro Gly Ile Pro Glu Thr Ala Ser Val Val Ala Ile Thr Val
 155 160 165
 Gln Glu Leu Phe Pro Ala Pro Ile Leu Arg Ala Val Pro Ser Ala
 170 175 180
 Glu Pro Gln Ala Gly Ser Pro Met Thr Leu Ser Cys Gln Thr Lys
 185 190 195

Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	200	205	210
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	215	220	225
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	230	235	240
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	245	250	255
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	260	265	270
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	275	280	285
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	290	295	300
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	305	310	315
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	320	325	330
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	335	340	345
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		350	355	

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<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

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<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 47

tttcagcgc caattctc 18

<210> 48

<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 48
agttcttgga ctgtgatagc cac 23

<210> 49
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 49
aaacttggtt gtcctcagtg gctg 24

<210> 50
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 50
gtgagggaacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51
<211> 2181
<212> DNA
<213> Homo sapiens

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<210> 52
 <211> 321
 <212> PRT
 <213> Homo sapiens

<400> 52
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 35 40 45
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg
 50 55 60
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp
 65 70 75
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His
 80 85 90
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met
 95 100 105
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro
 110 115 120
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val
 125 130 135
 Gln Lys Leu Ser Val Ser Lys Pro Thr Tyr Ile Thr Gly Ser Lys
 140 145 150
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys
 155 160 165
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln
 170 175 180
 Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr Leu Ser Thr
 185 190 195

Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser	Tyr	Phe	200	205	210
Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	Ile	215	220	225
Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	230	235	240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	245	250	255
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	260	265	270
Leu	Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	275	280	285
Ala	Ile	Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	290	295	300
Met	Ala	Tyr	Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	305	310	315
Val	Tyr	Glu	Ala	Ala	Arg										320		

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 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 53
 tatccctcca attgagcacc ctgg 24

<210> 54
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 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 54
 jcttgagagc atcccaacaa g 24

<210> 55
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 55
cttcacaatg tcgctgtgct gctc 24

<210> 56
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 56
agccaaatcc agcagctggc ttac 24

<210> 57
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<220>
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tggatgaccg gagccactac acgtgtgaaq tcacctggca gactcctgat 50

<210> 58
<211> 2458
<212> DNA
<213> Homo sapiens

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	185	190	195
Gln Asn Leu Thr	Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr	Ala
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Gly Asn Glu Ala	Gly Lys Glu Ser Cys	Val Val Arg Val Thr	Val
	215	220	225
Gln Tyr Val Gln	Ser Ile Gly Met Val	Ala Gly Ala Val Thr	Gly
	230	235	240
Ile Val Ala Gly	Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu	Leu
	245	250	255
Ile Arg Arg Lys	Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg	Pro
	260	265	270
Asn Glu Ile Arg	Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu	Val
	275	280	285
Lys Pro Ser Ser	Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser	Gly
	290	295	300
Ser Ser Ser Thr	Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser	Gln
	305	310	315
Arg Thr Leu Ser	Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala	Thr
	320	325	330
Gln Ala Tyr Ser	Leu Val Gly Pro Glu	Val Arg Gly Ser Glu	Pro
	335	340	345
Lys Lys Val His	His Ala Asn Leu Thr	Lys Ala Glu Thr Thr	Pro
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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 61

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 61

actaggtgt atgctgggt gggc 24

<210> 62

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 62

gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63

<211> 3534

<212> DNA

<213> Homo sapiens

<400> 63

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 <211> 655
 <212> PRT
 <213> Homo sapiens

<400> 64

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Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln		35	40	45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala		50	55	60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr		65	70	75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser		80	85	90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys		95	100	105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys		110	115	120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro		125	130	135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys		140	145	150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp		155	160	165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro		170	175	180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln		185	190	195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val		200	205	210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro		215	220	225	
Gly	Thr	Ala	Ile	Ile	Pro	Arg	Pro	Gln	His	Met	Gln	Thr	Gln	Gln		230	235	240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu		245	250	255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile		260	265	270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys		275	280	285	

Glu Asp Val Asn Lys Thr Leu Pro Asn Leu Gln Val Val Asn His	290	295	300
Gln Gln Gly Pro His His Arg His Ile Leu Lys Leu Leu Pro Ser	305	310	315
Met Glu Ala Thr Gly Gly Glu Lys Ser Ser Thr Pro Ile Lys Gly	320	325	330
Pro Lys Arg Gly His Pro Arg Gln Asn Leu His Lys His Phe Asp	335	340	345
Ile Asn Glu His Leu Pro Trp Met Ile Val Leu Phe Leu Leu Leu	350	355	360
Val Leu Val Val Ile Val Val Cys Ser Ile Arg Lys Ser Ser Arg	365	370	375
Thr Leu Lys Lys Gly Pro Arg Gln Asp Pro Ser Ala Ile Val Glu	380	385	390
Lys Ala Gly Leu Lys Lys Ser Met Thr Pro Thr Gln Asn Arg Glu	395	400	405
Lys Trp Ile Tyr Tyr Cys Asn Gly His Gly Ile Asp Ile Leu Lys	410	415	420
Leu Val Ala Ala Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr Gln	425	430	435
Phe Leu Cys Asn Ala Ser Glu Arg Glu Val Ala Ala Phe Ser Asn	440	445	450
Gly Tyr Thr Ala Asp His Glu Arg Ala Tyr Ala Ala Leu Gln His	455	460	465
Trp Thr Ile Arg Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile Ser	470	475	480
Ala Leu Arg Gln His Arg Arg Asn Asp Val Val Glu Lys Ile Arg	485	490	495
Gly Leu Met Glu Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu Ala	500	505	510
Leu Phe Met Ser Phe Phe Phe Leu Ser Phe Ser Phe Ile Phe Ser	515	520	525
Pro Asn Ala Lys Leu Glu Asn Ser Ala Leu Leu Thr Val Glu Pro	530	535	540
Ser Pro Gln Asp Lys Asn Lys Gly Phe Phe Val Asp Glu Ser Glu	545	550	555
Pro Leu Leu Arg Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala Leu	560	565	570

Ser	Arg	Asn	Gly	Ser	Phe	Ile	Thr	Lys	Glu	Lys	Lys	Asp	Thr	Val
				575					580					585
Leu	Arg	Gln	Val	Arg	Leu	Asp	Pro	Cys	Asp	Leu	Gln	Pro	Ile	Phe
				590					595					600
Asp	Asp	Met	Leu	His	Phe	Leu	Asn	Pro	Glu	Glu	Leu	Arg	Val	Ile
				605					610					615
Glu	Glu	Ile	Pro	Gln	Ala	Glu	Asp	Lys	Leu	Asp	Arg	Leu	Phe	Glu
				620					625					630
Ile	Ile	Gly	Val	Lys	Ser	Gln	Glu	Ala	Ser	Gln	Thr	Leu	Leu	Asp
				635					640					645
Ser	Val	Tyr	Ser	His	Leu	Pro	Asp	Leu	Leu					
				650					655					

<210> 65

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 65

gtagcagtgc acatggggtg ttgg 24

<210> 66

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 66

gacgcacatc ctcagtcctc gtcc 24

<210> 67

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 67

agatgatcg cgggtacat tctctggtt ggattactta ggaacacaa 50

<210> 68

<211> 2412

<212> DNA

<213> Homo sapiens

<400> 68

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ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200
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<210> 69

<211> 453

<212> 187

<213> Homo sapiens

<400> 69

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Arg	Ser	Leu	Phe	Gly	Leu	Asp	Asp	Leu	Lys	Ile	Ser	Pro	Val	Ala
				20				25						30

Pro	Asp	Ala	Asp	Ala	Val	Ala	Ala	Gln	Ile	Leu	Ser	Leu	Leu	Pro
				35				40						45

Leu	Lys	Phe	Phe	Pro	Ile	Ile	Val	Ile	Gly	Ile	Ile	Ala	Leu	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly	65		70		75
Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala	80		85		90
Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr	95		100		105
Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe	110		115		120
Thr Ala Ala Ser Trp Lys Thr Met Cys Ser Asp Asp Trp Lys Gly	125		130		135
His Tyr Ala Asn Val Ala Cys Ala Gln Leu Gly Phe Pro Ser Tyr	140		145		150
Val Ser Ser Asp Asn Leu Arg Val Ser Ser Leu Glu Gly Gln Phe	155		160		165
Arg Glu Glu Phe Val Ser Ile Asp His Leu Leu Pro Asp Asp Lys	170		175		180
Val Thr Ala Leu His His Ser Val Tyr Val Arg Glu Gly Cys Ala	185		190		195
Ser Gly His Val Val Thr Leu Gln Cys Thr Ala Cys Gly His Arg	200		205		210
Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met Ser Leu Leu	215		220		225
Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly Tyr His	230		235		240
Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr Ala	245		250		255
Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile	260		265		270
Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His	275		280		285
Leu Val Gly Tyr Ile Val Tyr His Gln Tyr Tyr Tyr Pro Tyr Arg	290		295		300
Leu Gly Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr	305		310		315
Phe Asn Glu Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu	320		325		330
Asn Phe Pro Asp Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala					

	335	340	345
Thr Glu Asp Gly	Gly Asp Ala Ser Pro	Val Leu Asn His Ala	Ala
	350	355	360
Val Pro Leu Ile	Ser Asn Lys Ile Cys	Asn His Arg Asp Val	Tyr
	365	370	375
Gly Gly Ile Ile	Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu	Thr
	380	385	390
Gly Gly Val Asp	Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu	Val
	395	400	405
Cys Gln Glu Arg	Arg Leu Trp Lys Leu	Val Gly Ala Thr Ser	Phe
	410	415	420
Gly Ile Gly Cys	Ala Glu Val Asn Lys	Pro Gly Val Tyr Thr	Arg
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Val Thr Ser Phe	Leu Asp Trp Ile His	Glu Gln Met Glu Arg	Asp
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<210> 70
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 70
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<210> 71
 <211> 24
 <212> DNA
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<220>
 <223> Synthetic oligonucleotide probe

<400> 71
 taccgtccc tgtggttgca gac 24

<210> 72
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 72

cgttcaatgc agaaatgata cagcctgtgt gcctgcccaa ctctgaagag 50

<210> 73

<211> 3305

<212> DNA

<213> Homo sapiens

<400> 73

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<210> 74

<211> 735

<212> PRT

<213> Homo sapiens

<400> 74

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Leu	Ala	Leu	Ala	Gly	Ala	Leu	Leu	Ala	Pro	Cys	Glu	Ala	Arg	Gly
				20					25					30
Val	Ser	Leu	Trp	Asn	Gln	Gly	Arg	Ala	Asp	Glu	Val	Val	Ser	Ala
				35					40					45
Ser	Val	Arg	Ser	Gly	Asp	Leu	Trp	Ile	Pro	Val	Lys	Ser	Phe	Asp
				50					55					60
Ser	Lys	Asn	His	Pro	Glu	Val	Leu	Asn	Ile	Arg	Leu	Gln	Arg	Glu
				65					70					75
Ser	Lys	Glu	Leu	Ile	Ile	Asn	Leu	Glu	Arg	Asn	Glu	Gly	Leu	Ile
				80					85					90
Ala	Ser	Ser	Phe	Thr	Glu	Thr	His	Tyr	Leu	Gln	Asp	Gly	Thr	Asp
				95					100					105
Val	Ser	Leu	Ala	Arg	Asn	Tyr	Thr	Gly	His	Cys	Tyr	Tyr	His	Gly
				110					115					120

His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys	125	130	135
Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val	140	145	150
Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro	155	160	165
Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His	170	175	180
Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser	185	190	195
Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr	200	205	210
Lys Tyr Val Glu Leu Val Ile Val Ala Asp Asn Arg Glu Phe Gln	215	220	225
Arg Gln Gly Lys Asp Leu Glu Lys Val Lys Gln Arg Leu Ile Glu	230	235	240
Ile Ala Asn His Val Asp Lys Phe Tyr Arg Pro Leu Asn Ile Arg	245	250	255
Ile Val Leu Val Gly Val Glu Val Trp Asn Asp Met Asp Lys Cys	260	265	270
Ser Val Ser Gln Asp Pro Phe Thr Ser Leu His Glu Phe Leu Asp	275	280	285
Trp Arg Lys Met Lys Leu Leu Pro Arg Lys Ser His Asp Asn Ala	290	295	300
Gln Leu Val Ser Gly Val Tyr Phe Gln Gly Thr Thr Ile Gly Met	305	310	315
Ala Pro Ile Met Ser Met Cys Thr Ala Asp Gln Ser Gly Gly Ile	320	325	330
Val Met Asp His Ser Asp Asn Pro Leu Gly Ala Ala Val Thr Leu	335	340	345
Ala His Glu Leu Gly His Asn Phe Gly Met Asn His Asp Thr Leu	350	355	360
Asp Arg Gly Cys Ser Cys Gln Met Ala Val Glu Lys Gly Gly Cys	365	370	375
Ile Met Asn Ala Ser Thr Gly Tyr Pro Phe Pro Met Val Phe Ser	380	385	390
Ser Cys Ser Arg Lys Asp Leu Glu Thr Ser Leu Glu Lys Gly Met	395	400	405

Gly Val Cys Leu Phe Asn Leu Pro Glu Val Arg Glu Ser Phe Gly	410	415	420
Gly Gln Lys Cys Gly Asn Arg Phe Val Glu Glu Gly Glu Glu Cys	425	430	435
Asp Cys Gly Glu Pro Glu Glu Cys Met Asn Arg Cys Cys Asn Ala	440	445	450
Thr Thr Cys Thr Leu Lys Pro Asp Ala Val Cys Ala His Gly Leu	455	460	465
Cys Cys Glu Asp Cys Gln Leu Lys Pro Ala Gly Thr Ala Cys Arg	470	475	480
Asp Ser Ser Asn Ser Cys Asp Leu Pro Glu Phe Cys Thr Gly Ala	485	490	495
Ser Pro His Cys Pro Ala Asn Val Tyr Leu His Asp Gly His Ser	500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr Asn Gly Ile Cys Gln Thr	515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp Gly Pro Gly Ala Lys Pro	530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val Asn Ser Ala Gly Asp Pro	545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys Ser Ser Phe Ala Lys Cys	560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys Ile Gln Cys Gln Gly Gly	575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn Ala Val Ser Ile Glu Thr	590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg Ile Leu Cys Arg Gly Thr	605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro Asp Pro Gly Leu Val Leu	620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys Ile Cys Leu Asn Arg Gln	635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val His Glu Cys Ala Met Gln	650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn Arg Lys Asn Cys His Cys	665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys Asp Lys Phe Gly Phe Gly	680	685	690

Gly Ser Thr Asp Ser Gly Pro Ile Arg Gln Ala Glu Ala Arg Gln
695 700 705

Glu Ala Ala Glu Ser Asn Arg Glu Arg Gly Gln Gly Gln Glu Pro
710 715 720

Val Gly Ser Gln Glu His Ala Ser Thr Ala Ser Leu Thr Leu Ile
725 730 735

<210> 75

<211> 483

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473

<223> unknown base

<400> 75

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ctgacaacga aaacaaaaca gttttgggga ttccaggagg gaantccagc 100

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ttgagntttt tgntaaaaca tggacatgnt tcagtgtgc tcntgagaga 200

gtagcaggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250

aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300

aggaagggtt gggcccagtg tcccctttcc ccagtgcac ctcagccttg 350

gcagccctga taactggtnt ntgggtgcaa nttaatgctn tgatatggt 400

tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450

gagaccctgc caccattcc atntccatcc aag 483

<210> 76

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 76

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<210> 77

<211> 18

<212> DNA

<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 77
catgagcatg tgcacggc 18

<210> 78
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 78
tacctgcacg atgggcac 18

<210> 79
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 79
caatgggcac ctcccttc 18

<210> 80
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 80
ctccaggctg gtctccaagt ccttcc 26

<210> 81
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<212> DNA
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<220>
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<400> 81
tgaatgattga actctacagg ttcc 24

<210> 82
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
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<400> 82
cttcgctggg aagagtttg 19

<210> 83
<211> 50
<212> DNA
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<220>
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<400> 83
gtgcaaccaa cagatacaaa ctcttccag cgaagaagct gaaaagcgtc 50

<210> 84
<211> 1714
<212> DNA
<213> Homo sapiens

<400> 84
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atgatctgcc cgctcgggcc tcccaaagtg ctgggattac aggcgagtgc 150
aacacacccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200
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<210> 85
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 85
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 20 25 30
 Thr Ser Met Pro Gln Ala Thr Ala Ala Gln Thr Thr Lys Pro Ser
 35 40 45
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu
 50 55 60
 Ala Leu Leu His Leu Tyr His
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<210> 86
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 86
acgggcacac tggatcccaa atg 23

<210> 87
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 87
ggtagagatg tagaagggca agcaagacc 29

<210> 88
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 88
gctccctacc cgtgcagggt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89
<211> 2956
<212> DNA
<213> Homo sapiens

<400> 89
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aggggggggc gacacacacg gacggggccc ccgcggcaga cggcgaaggac 200
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cgggataccag agcgccgcgc acttcgtcat gttcttcggg cactgggtgtg 300
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<210> 90

<211> 432

<212> PRT

<213> Homo sapiens

<400> 90

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Ala	Ala	Leu	Thr	Ala	Leu	Leu	Leu	Leu	Leu	Gly	His	Gly	Gly
				20					25				30

Gly	Gly	Arg	Trp	Gly	Ala	Arg	Ala	Gln	Glu	Ala	Ala	Ala	Ala	Ala
				35					40					45

Ala Asp Gly Pro	Pro Ala Ala Asp Gly	Glu Asp Gly Gln Asp	Pro
50		55	60
His Ser Lys His	Leu Tyr Thr Ala Asp	Met Phe Thr His Gly	Ile
65		70	75
Gln Ser Ala Ala	His Phe Val Met Phe	Phe Ala Pro Trp Cys	Gly
80		85	90
His Cys Gln Arg	Leu Gln Pro Thr Trp	Asn Asp Leu Gly Asp	Lys
95		100	105
Tyr Asn Ser Met	Glu Asp Ala Lys Val	Tyr Val Ala Lys Val	Asp
110		115	120
Cys Thr Ala His	Ser Asp Val Cys Ser	Ala Gln Gly Val Arg	Gly
125		130	135
Tyr Pro Thr Leu	Lys Leu Phe Lys Pro	Gly Gln Glu Ala Val	Lys
140		145	150
Tyr Gln Gly Pro	Arg Asp Phe Gln Thr	Leu Glu Asn Trp Met	Leu
155		160	165
Gln Thr Leu Asn	Glu Glu Pro Val Thr	Pro Glu Pro Glu Val	Glu
170		175	180
Pro Pro Ser Ala	Pro Glu Leu Lys Gln	Gly Leu Tyr Glu Leu	Ser
185		190	195
Ala Ser Asn Phe	Glu Leu His Val Ala	Gln Gly Asp His Phe	Ile
200		205	210
Lys Phe Phe Ala	Pro Trp Cys Gly His	Cys Lys Ala Leu Ala	Pro
215		220	225
Thr Trp Glu Gln	Leu Ala Leu Gly Leu	Glu His Ser Glu Thr	Val
230		235	240
Lys Ile Gly Lys	Val Asp Cys Thr Gln	His Tyr Glu Leu Cys	Ser
245		250	255
Gly Asn Gln Val	Arg Gly Tyr Pro Thr	Leu Leu Trp Phe Arg	Asp
260		265	270
Gly Lys Lys Val	Asp Gln Tyr Lys Gly	Lys Arg Asp Leu Glu	Ser
275		280	285
Leu Arg Glu Tyr	Val Glu Ser Gln Leu	Gln Arg Thr Glu Thr	Gly
290		295	300
Ala Thr Glu Thr	Val Thr Pro Ser Glu	Ala Pro Val Leu Ala	Ala
305		310	315
Glu Pro Glu Ala	Asp Lys Gly Thr Val	Leu Ala Leu Thr Glu	Asn
320		325	330

Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe
				335					340					345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp
				350					355					360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys
				365					370					375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys
				380					385					390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly
				395					400					405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu
				410					415					420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu			
				425					430					

<210> 91
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 91
 atgttcctcg cgccctgggtg 20

<210> 92
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 92
 cttaagcgaac acactctaca a 21

<210> 93
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 93
 aaagtggctgc cttgtgcaac gtgc 24

<210> 94
 <211> 23

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 94
gggtcaaaggg gatatatcgc cac 23

<210> 95
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 95
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96
<211> 1016
<212> DNA
<213> Homo sapiens

<400> 96
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gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150
atttcaccag gacccaaaagg agatgatggg gaaaaaggag atccaggaga 200
agagggaaaag catggcaaag tgggacgcat gggggccgaaa ggaattaaag 250
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 aaaaaaaaaa aaaaaa 1016

<210> 97
 <211> 277
 <212> PRT
 <213> Homo sapiens

<400> 97
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 20 25 30
 Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser
 35 40 45
 Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu
 50 55 60
 Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile
 65 70 75
 Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys
 80 85 90
 Thr Gly Pro Ile Gly Lys Lys Gly Asp Lys Gly Glu Lys Gly Leu
 95 100 105
 Leu Gly Ile Pro Gly Glu Lys Gly Lys Ala Gly Thr Val Cys Asp
 110 115 120
 Cys Gly Arg Tyr Arg Lys Phe Val Gly Gln Leu Asp Ile Ser Ile
 125 130 135
 Ala Arg Leu Lys Thr Ser Met Lys Phe Val Lys Asn Val Ile Ala
 140 145 150
 Gly Ile Arg Glu Thr Glu Glu Lys Phe Tyr Tyr Ile Val Gln Glu
 155 160 165
 Glu Lys Asn Tyr Arg Glu Ser Leu Thr His Cys Arg Ile Arg Gly
 170 175 180
 Gly Met Leu Ala Met Pro Lys Asp Glu Ala Ala Asn Thr Leu Ile
 185 190 195
 Ala Asp Tyr Val Ala Lys Ser Gly Phe Phe Arg Val Phe Ile Gly

	200		205		210
Val Asn Asp Leu Glu Arg Glu Gly Gln Tyr Met Ser Thr Asp Asn					
	215		220		225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp Asn Glu Gly Glu Pro Ser					
	230		235		240
Asp Pro Tyr Gly His Glu Asp Cys Val Glu Met Leu Ser Ser Gly					
	245		250		255
Arg Trp Asn Asp Thr Glu Cys His Leu Thr Met Tyr Phe Val Cys					
	260		265		270
Glu Phe Ile Lys Lys Lys Lys					
	275				

<210> 98
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 98
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<210> 99
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 99
 gatgatggag gctccatacc tcag 24

<210> 100
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 100
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<210> 101
 <211> 2574
 <212> DNA
 <213> Homo sapiens

<400> 101
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<211> 730

<212> PRT

<213> Homo sapiens

<400> 102

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Gln	Leu	Glu	Arg	Ala	Ala	Leu	Gly	Phe	Arg	Lys	Gly	Gly	Ser	Gly
				20					25					30

Met	Phe	Ala	Ser	Gly	Trp	Asn	Gln	Thr	Val	Pro	Ile	Glu	Glu	Ala	35	40	45
Gly	Ser	Met	Ala	Ala	Leu	Leu	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	50	55	60
Pro	Leu	Leu	Leu	Leu	Lys	Leu	His	Leu	Trp	Pro	Gln	Leu	Arg	Trp	65	70	75
Leu	Pro	Ala	Asp	Leu	Ala	Phe	Ala	Val	Arg	Ala	Leu	Cys	Cys	Lys	80	85	90
Arg	Ala	Leu	Arg	Ala	Arg	Ala	Leu	Ala	Ala	Ala	Ala	Ala	Asp	Pro	95	100	105
Glu	Gly	Pro	Glu	Gly	Gly	Cys	Ser	Leu	Ala	Trp	Arg	Leu	Ala	Glu	110	115	120
Leu	Ala	Gln	Gln	Arg	Ala	Ala	His	Thr	Phe	Leu	Ile	His	Gly	Ser	125	130	135
Arg	Arg	Phe	Ser	Tyr	Ser	Glu	Ala	Glu	Arg	Glu	Ser	Asn	Arg	Ala	140	145	150
Ala	Arg	Ala	Phe	Leu	Arg	Ala	Leu	Gly	Trp	Asp	Trp	Gly	Pro	Asp	155	160	165
Gly	Gly	Asp	Ser	Gly	Glu	Gly	Ser	Ala	Gly	Glu	Gly	Glu	Arg	Ala	170	175	180
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Ala	Gly	Gly	Asp	Gly	Ala	Ala	Arg	Gly	Gly	Gly	Ala	Ala	Ala	Pro	200	205	210
Leu	Ser	Pro	Gly	Ala	Thr	Val	Ala	Leu	Leu	Leu	Pro	Ala	Gly	Pro	215	220	225
Glu	Phe	Leu	Trp	Leu	Trp	Phe	Gly	Leu	Ala	Lys	Ala	Gly	Leu	Arg	230	235	240
Thr	Ala	Phe	Val	Pro	Thr	Ala	Leu	Arg	Arg	Gly	Pro	Leu	Leu	His	245	250	255
Cys	Leu	Arg	Ser	Cys	Gly	Ala	Arg	Ala	Leu	Val	Leu	Ala	Pro	Glu	260	265	270
Phe	Leu	Glu	Ser	Leu	Glu	Pro	Asp	Leu	Pro	Ala	Leu	Arg	Ala	Met	275	280	285
Gly	Leu	His	Leu	Trp	Ala	Ala	Gly	Pro	Gly	Thr	His	Pro	Ala	Gly	290	295	300
Ile	Ser	Asp	Leu	Leu	Ala	Glu	Val	Ser	Ala	Glu	Val	Asp	Gly	Pro	305	310	315

Val Pro Gly Tyr	Leu Ser Ser Pro Gln	Ser Ile Thr Asp Thr	Cys
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Leu Tyr Ile Phe	Thr Ser Gly Thr Thr	Gly Leu Pro Lys Ala	Ala
335	340		345
Arg Ile Ser His	Leu Lys Ile Leu Gln	Cys Gln Gly Phe Tyr	Gln
350	355		360
Leu Cys Gly Val	His Gln Glu Asp Val	Ile Tyr Leu Ala Leu	Pro
365	370		375
Leu Tyr His Met	Ser Gly Ser Leu Leu	Gly Ile Val Gly Cys	Met
380	385		390
Gly Ile Gly Ala	Thr Val Val Leu Lys	Ser Lys Phe Ser Ala	Gly
395	400		405
Gln Phe Trp Glu	Asp Cys Gln Gln His	Arg Val Thr Val Phe	Gln
410	415		420
Tyr Ile Gly Glu	Leu Cys Arg Tyr Leu	Val Asn Gln Pro Pro	Ser
425	430		435
Lys Ala Glu Arg	Gly His Lys Val Arg	Leu Ala Val Gly Ser	Gly
440	445		450
Leu Arg Pro Asp	Thr Trp Glu Arg Phe	Val Arg Arg Phe Gly	Pro
455	460		465
Leu Gln Val Leu	Glu Thr Tyr Gly Leu	Thr Glu Gly Asn Val	Ala
470	475		480
Thr Ile Asn Tyr	Thr Gly Gln Arg Gly	Ala Val Gly Arg Ala	Ser
485	490		495
Trp Leu Tyr Lys	His Ile Phe Pro Phe	Ser Leu Ile Arg Tyr	Asp
500	505		510
Val Thr Thr Gly	Glu Pro Ile Arg Asp	Pro Gln Gly His Cys	Met
515	520		525
Ala Thr Ser Pro	Gly Glu Pro Gly Leu	Leu Val Ala Pro Val	Ser
530	535		540
Gln Gln Ser Pro	Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu	Ala
545	550		555
Gln Gly Lys Leu	Leu Lys Asp Val Phe	Arg Pro Gly Asp Val	Phe
560	565		570
Phe Asn Thr Gly	Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe	Leu
575	580		585
Arg Phe His Asp	Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly	Glu
590	595		600

Asn Val Ala Thr Thr Glu Val Ala Glu Val Phe Glu Ala Leu Asp	605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly Val Thr Val Pro Gly His	620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu Val Leu Arg Pro Pro His	635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr His Val Ser Glu Asn Leu	650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu Arg Leu Gln Glu Ser Leu	665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln Lys Val Arg Met Ala Asn	680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser Asp Pro Leu Tyr Val Leu	695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro Leu Thr Thr Ala Arg Tyr	710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg Ile	725	730	

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 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

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<210> 104
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 <212> DNA
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<220>
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<400> 104
 jggagaaagtg ggcacaaac 18

<210> 105
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 <223> Synthetic oligonucleotide probe

<400> 105
gccctggcac agtgactcca tagacg 26

<210> 106
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<220>
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<400> 106
atccacttca gcggacac 18

<210> 107
<211> 45
<212> DNA
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<220>
<223> Synthetic oligonucleotide probe

<400> 107
cagtgccag gataactata ttccccccag agcataacag acacg 45

<210> 108
<211> 2579
<212> DNA
<213> Homo sapiens

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ccggcgcgcg ctcccacctt tgcgcacac tccggcgagc cgagcccgca 200
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<210> 109

<211> 555

<212> PRT

<213> Homo sapiens

<400> 109

Met	Pro	Ser	Trp	Ile	Gly	Ala	Val	Ile	Leu	Pro	Leu	Leu	Gly	Leu	1	5	10	15
Leu	Leu	Ser	Leu	Pro	Ala	Gly	Ala	Asp	Val	Lys	Ala	Arg	Ser	Cys	20	25	30	
Gly	Glu	Val	Arg	Gln	Ala	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ala	35	40	45	
Asp	Ile	Pro	Tyr	Gln	Glu	Ile	Ala	Gly	Glu	His	Leu	Arg	Ile	Cys	50	55	60	
Pro	Gln	Glu	Tyr	Thr	Cys	Cys	Thr	Thr	Glu	Met	Glu	Asp	Lys	Leu	65	70	75	
Ser	Gln	Gln	Ser	Lys	Ile	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90	
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105	
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120	
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135	
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150	

Thr Gly Gly Asn Val Asn Leu Glu Glu Met Leu Asn Asp Phe Trp	155	160	165
Ala Arg Leu Leu Glu Arg Met Phe Gln Leu Ile Asn Pro Gln Tyr	170	175	180
His Phe Ser Glu Asp Tyr Leu Glu Cys Val Ser Lys Tyr Thr Asp	185	190	195
Gln Leu Lys Pro Phe Gly Asp Val Pro Arg Lys Leu Lys Ile Gln	200	205	210
Val Thr Arg Ala Phe Ile Ala Ala Arg Thr Phe Val Gln Gly Leu	215	220	225
Thr Val Gly Arg Glu Val Ala Asn Arg Val Ser Lys Val Ser Pro	230	235	240
Thr Pro Gly Cys Ile Arg Ala Leu Met Lys Met Leu Tyr Cys Pro	245	250	255
Tyr Cys Arg Gly Leu Pro Thr Val Arg Pro Cys Asn Asn Tyr Cys	260	265	270
Leu Asn Val Met Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp	275	280	285
Thr Glu Trp Asn Leu Phe Ile Asp Ala Met Leu Leu Val Ala Glu	290	295	300
Arg Leu Glu Gly Pro Phe Asn Ile Glu Ser Val Met Asp Pro Ile	305	310	315
Asp Val Lys Ile Ser Glu Ala Ile Met Asn Met Gln Glu Asn Ser	320	325	330
Met Gln Val Ser Ala Lys Val Phe Gln Gly Cys Gly Gln Pro Lys	335	340	345
Pro Ala Pro Ala Leu Arg Ser Ala Arg Ser Ala Pro Glu Asn Phe	350	355	360
Asn Thr Arg Phe Arg Pro Tyr Asn Pro Glu Glu Arg Pro Thr Thr	365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu Val Thr Asp Ile Lys Glu	380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp Ser Ala Leu Pro Tyr Thr	395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala Gly Thr Ser Asn Glu Glu	410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala Arg Tyr Leu Pro Glu Ile	425	430	435

Met	Asn	Asp	Gly	Leu	Thr	Asn	Gln	Ile	Asn	Asn	Pro	Glu	Val	Asp
				440					445					450
Val	Asp	Ile	Thr	Arg	Pro	Asp	Thr	Phe	Ile	Arg	Gln	Gln	Ile	Met
				455					460					465
Ala	Leu	Arg	Val	Met	Thr	Asn	Lys	Leu	Lys	Asn	Ala	Tyr	Asn	Gly
				470					475					480
Asn	Asp	Val	Asn	Phe	Gln	Asp	Thr	Ser	Asp	Glu	Ser	Ser	Gly	Ser
				485					490					495
Gly	Ser	Gly	Ser	Gly	Cys	Met	Asp	Asp	Val	Cys	Pro	Thr	Glu	Phe
				500					505					510
Glu	Phe	Val	Thr	Thr	Glu	Ala	Pro	Ala	Val	Asp	Pro	Asp	Arg	Arg
				515					520					525
Glu	Val	Asp	Ser	Ser	Ala	Ala	Gln	Arg	Gly	His	Ser	Leu	Leu	Ser
				530					535					540
Trp	Ser	Leu	Thr	Cys	Ile	Val	Leu	Ala	Leu	Gln	Arg	Leu	Cys	Arg
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<210> 110
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 <223> Synthetic oligonucleotide probe

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<210> 111
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 111
 agcacagtct ctgcagtggc cagg 24

<210> 112
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 <213> Artificial Sequence

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<400> 112
 gaatgctgga acgggcacag caaagccaga tacttgctg 40

<210> 113
<211> 4649
<212> DNA
<213> Homo sapiens

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cgccaactac gcaaagacca agcgggctcc gcgcggaccg gccgcggggc 150
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<210> 114
 <211> 515
 <212> PRT
 <213> Homo sapiens

<400> 114

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Ala	Gly	Phe	Trp	Ile	Leu	Cys	Leu	Leu	Thr	Tyr	Gly	Tyr	Leu	Ser	35	40	45	
Trp	Gly	Gln	Ala	Leu	Glu	Glu	Glu	Glu	Glu	Gly	Ala	Leu	Leu	Ala	50	55	60	
Gln	Ala	Gly	Glu	Lys	Leu	Glu	Pro	Ser	Thr	Thr	Ser	Thr	Ser	Gln	65	70	75	
Pro	His	Leu	Ile	Phe	Ile	Leu	Ala	Asp	Asp	Gln	Gly	Phe	Arg	Asp	80	85	90	
Val	Gly	Tyr	His	Gly	Ser	Glu	Ile	Lys	Thr	Pro	Thr	Leu	Asp	Lys	95	100	105	
Leu	Ala	Ala	Glu	Gly	Val	Lys	Leu	Glu	Asn	Tyr	Tyr	Val	Gln	Pro	110	115	120	
Ile	Cys	Thr	Pro	Ser	Arg	Ser	Gln	Phe	Ile	Thr	Gly	Lys	Tyr	Gln	125	130	135	
Ile	His	Thr	Gly	Leu	Gln	His	Ser	Ile	Ile	Arg	Pro	Thr	Gln	Pro	140	145	150	

Asn Cys Leu Pro	Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	155	160	165
Glu Val Gly Tyr	Ser Thr His Met Val	Gly Lys Trp His Leu Gly	170	175	180
Phe Asn Arg Lys	Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	185	190	195
Phe Phe Gly Ser	Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	200	205	210
Lys Cys Asp Ser	Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	215	220	225
Asp Asn Ala Ala	Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	230	235	240
Met Tyr Thr Gln	Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	245	250	255
Thr Lys Pro Ile	Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	260	265	270
Pro Leu Gln Ala	Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	275	280	285
Ile Asn Ile Asn	Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	290	295	300
Asp Glu Ala Ile	Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	305	310	315
Phe Tyr Asn Asn	Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	320	325	330
Gln Pro Thr Ala	Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	335	340	345
Gly Thr Tyr Trp	Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	350	355	360
Ser Pro Leu Leu	Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	365	370	375
His Ile Thr Asp	Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	380	385	390
Gln Ile Asp Glu	Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	395	400	405
Thr Ile Ser Glu	Gly Leu Arg Ser Pro	Arg Val Asp Ile Leu His	410	415	420
Asn Ile Asp Pro	Tyr Thr Pro Arg Gln	Lys Met Ala Pro Gly Gln	425	430	435

Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 115

cccaacccaa ctgtttacct ctgg 24

<210> 116

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 116

ctctctgagt gtacatctgt gtgg 24

<210> 117

<211> 53

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<220>

<221> unsure

<222> 33

<223> unknown base

<400> 117

ggcaccttac ctacagaaact gaaggaggtt ggntattcaa cgcatatggt 50

cgq 53

<210> 118

<211> 2260

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086

<223> unknown base

<400> 118

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gggctcagga ggaggaagga ggaccgctgc gagaatgcct ctgccctgga 150
gacttgccgt cccgctgctg ctctcctggg tggcaggtgg ttccgggaac 200
ggggccagtg caaggcatca cgggttggtta gcacggcac gtcagcctgg 250
ggctctgtac tatggaacta aactggcctg ctgtacggc tggagaagaa 300
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttgg 350
gagtgcgtgg gaccaaacia atgcagatgc ttccaggat acaccgggaa 400
aacctgcagt caagatgtga atgagtgtgg aatgaaacc cggccatgcc 450
aacacagatg tgtgaataca cacggaagct acaagtgctt ttgcctcagt 500
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550
catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600
gctgtgtcc atctcagga ctccgctgg ccccaaatgg aagagactgt 650
ctagatattg atqaatgtgc ctctggtaaa qtcactctgc cctacaatcg 700
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tgtactatgg atagcctac gtcaggtca atgtgact gttcctatc 850
ccaaggggtc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900
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tccagaggcg ggaactctca tggaggtaaa aaagggaatg aagagaaatg 1150
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 tgggatctgt gactggaac aggatagaga agatgatttt gactggaatc 1400
 ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450
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 gcaaccccaa agcaacttct gtttgcctt tgattaccgg ctggccggag 1550
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 aagtgctta gctggtctt tcatagcaa actgtatat ttaattctt 2250
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<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

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1				5					10					15

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	20	25	30
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	35	40	45
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	50	55	60
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	65	70	75
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	80	85	90
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	95	100	105
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	110	115	120
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	125	130	135
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	140	145	150
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	155	160	165
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	170	175	180
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	185	190	195
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	200	205	210
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	215	220	225
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	230	235	240
Gly	Ser	Phe	Lys	Lys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	245	250	255
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	260	265	270
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	275	280	285
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	290	295	300

Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro
305 310 315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys
335

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaaactgt cagtacagct gtgaagacac agaagaaggc ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gagagctgct gctgtggctg ctgggtgctgt ggcactact cctgctcttg 50

gtgcagctgc tgcgcttact gagggctgac ggcgaactga cgctactatg 100

ggccgagtggt cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtgggaattg gtgaggagct ggcttaccag 200

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<210> 124

<211> 289

<212> PRT

<213> Homo sapiens

<400> 124

Met	Val	Val	Trp	Val	Thr	Gly	Ala	Ser	Ser	Gly	Ile	Gly	Glu	Glu
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Leu	Ala	Tyr	Gln	Leu	Ser	Lys	Leu	Gly	Val	Ser	Leu	Val	Leu	Ser
				20					25					30

Ala	Arg	Arg	Val	His	Glu	Leu	Glu	Arg	Val	Lys	Arg	Arg	Cys	Leu
				35					40					45

Glu	Asn	Gly	Asn	Leu	Lys	Glu	Lys	Asp	Ile	Leu	Val	Leu	Pro	Leu
				50					55					60

Asp	Leu	Thr	Asp	Thr	Gly	Ser	His	Glu	Ala	Ala	Thr	Lys	Ala	Val	65	70	75
Leu	Gln	Glu	Phe	Gly	Arg	Ile	Asp	Ile	Leu	Val	Asn	Asn	Gly	Gly	80	85	90
Met	Ser	Gln	Arg	Ser	Leu	Cys	Met	Asp	Thr	Ser	Leu	Asp	Val	Tyr	95	100	105
Arg	Lys	Leu	Ile	Glu	Leu	Asn	Tyr	Leu	Gly	Thr	Val	Ser	Leu	Thr	110	115	120
Lys	Cys	Val	Leu	Pro	His	Met	Ile	Glu	Arg	Lys	Gln	Gly	Lys	Ile	125	130	135
Val	Thr	Val	Asn	Ser	Ile	Leu	Gly	Ile	Ile	Ser	Val	Pro	Leu	Ser	140	145	150
Ile	Gly	Tyr	Cys	Ala	Ser	Lys	His	Ala	Leu	Arg	Gly	Phe	Phe	Asn	155	160	165
Gly	Leu	Arg	Thr	Glu	Leu	Ala	Thr	Tyr	Pro	Gly	Ile	Ile	Val	Ser	170	175	180
Asn	Ile	Cys	Pro	Gly	Pro	Val	Gln	Ser	Asn	Ile	Val	Gln	Asn	Ser	185	190	195
Leu	Ala	Gly	Glu	Val	Thr	Lys	Thr	Ile	Gly	Asn	Asn	Gly	Asp	Gln	200	205	210
Ser	His	Lys	Met	Thr	Thr	Ser	Arg	Cys	Val	Arg	Leu	Met	Leu	Ile	215	220	225
Ser	Met	Ala	Asn	Asp	Leu	Lys	Glu	Val	Trp	Ile	Ser	Glu	Gln	Pro	230	235	240
Phe	Leu	Leu	Val	Thr	Tyr	Leu	Trp	Gln	Tyr	Met	Pro	Thr	Trp	Ala	245	250	255
Trp	Trp	Ile	Thr	Asn	Lys	Met	Gly	Lys	Lys	Arg	Ile	Glu	Asn	Phe	260	265	270
Lys	Ser	Gly	Val	Asp	Ala	Asp	Ser	Ser	Tyr	Phe	Lys	Ile	Phe	Lys	275	280	285
Thr	Lys	His	Asp														

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

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<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126

ctgtgaatag catcctggg 19

<210> 127

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127

cttttcaagc cactggaggg 20

<210> 128

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128

ctgtagacat ccaagctggg atcc 24

<210> 129

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129

ggtatga atcctggggtg 23

<210> 130

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130

acctgacgct actatgggcc gactggcagg gacgacgcc agaattg 46

<210> 131
<211> 2365
<212> DNA
<213> Homo sapiens

<400> 131
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<210> 132

<211> 571

<212> PRT

<213> Homo sapiens

<400> 132

Met	Leu	Leu	Ser	Ser	Leu	Val	Ser	Leu	Ala	Gly	Ser	Val	Tyr	Leu
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Ala	Trp	Ile	Leu	Phe	Phe	Val	Leu	Tyr	Asp	Phe	Cys	Ile	Val	Cys
			20					25						30

Ile Thr Thr Tyr Ala	Ile Asn Val Ser Leu Met Trp Leu Ser Phe	35	40	45
Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn		50	55	60
Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln		65	70	75
Gly Ala His Ile Cys Ser Gly Ser Leu Val Ala Asp Thr Trp Val		80	85	90
Leu Thr Ala Ala His Cys Phe Glu Lys Ala Ala Ala Thr Glu Leu		95	100	105
Asn Ser Trp Ser Val Val Leu Gly Ser Leu Gln Arg Glu Gly Leu		110	115	120
Ser Pro Gly Ala Glu Glu Val Gly Val Ala Ala Leu Gln Leu Pro		125	130	135
Arg Ala Tyr Asn His Tyr Ser Gln Gly Ser Asp Leu Ala Leu Leu		140	145	150
Gln Leu Ala His Pro Thr Thr His Thr Pro Leu Cys Leu Pro Gln		155	160	165
Pro Ala His Arg Phe Pro Phe Gly Ala Ser Cys Trp Ala Thr Gly		170	175	180
Trp Asp Gln Asp Thr Ser Asp Ala Pro Gly Thr Leu Arg Asn Leu		185	190	195
Arg Leu Arg Leu Ile Ser Arg Pro Thr Cys Asn Cys Ile Tyr Asn		200	205	210
Gln Leu His Gln Arg His Leu Ser Asn Pro Ala Arg Pro Gly Met		215	220	225
Leu Cys Gly Gly Pro Gln Pro Gly Val Gln Gly Pro Cys Gln Gly		230	235	240
Asp Ser Gly Gly Pro Val Leu Cys Leu Glu Pro Asp Gly His Trp		245	250	255
Val Gln Ala Gly Ile Ile Ser Phe Ala Ser Ser Cys Ala Gln		260	265	270
Asp Ala Pro Val Leu Leu Thr Asn Thr Ala Ala His Ser Ser Trp		275	280	285
Leu Gln Ala Arg Val Gln Gly Ala Ala Phe Leu Ala Gln Ser Pro		290	295	300
Glu Thr Pro Glu Met Ser Asp Gln Asp Ser Cys Val Ala Cys Gly		305	310	315

Ser Leu Arg Thr	Ala Gly Pro Gln Ala	Gly Ala Pro Ser Pro	Trp
320		325	330
Pro Trp Glu Ala	Arg Leu Met His Gln	Gly Gln Leu Ala Cys	Gly
335		340	345
Gly Ala Leu Val	Ser Glu Glu Ala Val	Leu Thr Ala Ala His	Cys
350		355	360
Phe Ile Gly Arg	Gln Ala Pro Glu Glu	Trp Ser Val Gly Leu	Gly
365		370	375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly
380		385	390
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu
395		400	405
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys
410		415	420
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp
425		430	435
Val Leu Glv Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln
440		445	450
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu
455		460	465
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met
470		475	480
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu
485		490	495
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu
500		505	510
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg
515		520	525
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser
530		535	540
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu
545		550	555
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser
560		565	570

Cys

<210> 133
 <211> 24
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcctc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggccgcgc ccggccccca ttcgggccgg gcctcgctgc ggcggcgact 50

gagccagggt gggccggctc cctgagtcgc agagtggcg cggcggcgca 100

ggggcagcct tccaccagg ggagcccagc tgcagccgc ctcacaggaa 150

gatgtgggt cggcgggga gccctggcat ggggtgtcat ggggggcag 200

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ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcctct 350

ggcagctgac agataccaaa cagctgggtgc acagctttgc tgagggcag 400

gaccagggca ggccttatgc caaccgcag gccctcttcc cggacctgct 450

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atgccttcag gatgtcatc ctccctgccc caggaaatgga agatgtgagg 1900
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attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> unsure
<222> 233
<223> unknown amino acid

<400> 137
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20 25 30
Val Gln Val Pro Glu Asp Pro Val Val Ala Leu Val Gly Thr Asp
35 40 45
Ala Thr Leu Cys Cys Ser Phe Ser Pro Glu Pro Gly Phe Ser Leu
50 55 60
Ala Gln Leu Asn Leu Ile Trp Gln Leu Thr Asp Thr Lys Gln Leu
65 70 75
Val His Ser Phe Ala Glu Gly Gln Asp Gln Gly Ser Ala Tyr Ala
80 85 90
Asn Arg Thr Ala Leu Phe Pro Asp Leu Leu Ala Gln Gly Asn Ala
95 100 105
Ser Leu Arg Leu Gln Arg Val Arg Val Ala Asp Glu Gly Ser Phe
110 115 120
Thr Cys Phe Val Ser Ile Arg Asp Phe Gly Ser Ala Ala Val Ser
125 130 135
Leu Gln Val Ala Ala Pro Tyr Ser Lys Pro Ser Met Thr Leu Glu
140 145 150
Pro Asn Lys Asp Leu Arg Pro Gly Asp Thr Val Thr Ile Thr Cys
155 160 165
Ser Ser Tyr Gln Gly Tyr Pro Glu Ala Gln Val Ile Thr Thr Arg
170 175 180
Gly Gln Gly Val Pro Leu Thr Gly Asn Val Thr Thr Ser Gln Met
185 190 195
Ala Asn Glu Gln Gly Leu Phe Asp Val His Ser Val Leu Arg Val
200 205 210
Val Leu Gly Ala Asn Gly Thr Tyr Ser Cys Leu Val Arg Asn Pro
215 220 225

Val	Leu	Gln	Gln	Asp	Ala	His	Xaa	Ser	Val	Thr	Ile	Thr	Gly	Gln	230	235	240
Pro	Met	Thr	Phe	Pro	Pro	Glu	Ala	Leu	Trp	Val	Thr	Val	Gly	Leu	245	250	255
Ser	Val	Cys	Leu	Ile	Ala	Leu	Leu	Val	Ala	Leu	Ala	Phe	Val	Cys	260	265	270
Trp	Arg	Lys	Ile	Lys	Gln	Ser	Cys	Glu	Glu	Glu	Asn	Ala	Gly	Ala	275	280	285
Glu	Asp	Gln	Asp	Gly	Glu	Gly	Glu	Gly	Ser	Lys	Thr	Ala	Leu	Gln	290	295	300
Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile	305	310	315

Ala

<210> 138

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 138

ctggcacagc tcaacatcat ctgg 24

<210> 139

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 139

tttatctgtc tgtctcattg 20

<210> 140

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 140

ttatctagta tatgacacac 20

<210> 141

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 141

tgcaaccag gcagctgtaa gtgc 24

<210> 142

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 142

tggaagaaga ggggtgtgat gtgg 24

<210> 143

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 143

gagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144

<211> 2336

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1620, 1673

<223> unknown base

<400> 144

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gaaggaggag ttgtgaatt gtcttaagat ttgtgtgtg agctttaccg 100

taagtcttta aatctatgaa gtgaggggac atttggctga ttgtgtggg 150

acttttttcc ttgcttcagc aacatgagga tttttttgtg gaagggggtc 200

ttgactctgt tcttcaatt tttgatgggg gctttgatcc ctgaaccaga 250

agtgaataatt gaagttctcc agaaqccatt catctgccat cgcaagacca 300

aaggaggggg ttgatgtgtg gtccactatg aaggtactt agaaaaggac 350

ggtctcttat ttaactccac tcacaaacat aacaatggtc agcccatctg 400

gtttaccctg ggcacccctg aggcctctcaa aggttgggac cagggcttga 450
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<210> 145

<211> 211

<212> PRT

<213> Homo sapiens

<400> 145

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Ser	Leu	Ile	Gly	Ala	Leu	Ile	Pro	Glu	Pro	Glu	Val	Lys	Ile	Glu
			20					25						30

Val	Leu	Gln	Lys	Pro	Phe	Ile	Cys	His	Arg	Lys	Thr	Lys	Gly	Gly
			35					40						45

Asp	Leu	Met	Leu	Val	His	Tyr	Glu	Gly	Tyr	Leu	Glu	Lys	Asp	Gly
			50					55						60

Ser	Leu	Phe	His	Ser	Thr	His	Lys	His	Asn	Asn	Gly	Gln	Pro	Ile
			65					70						75

Pro	Phe	Thr	Leu	Gly	Ile	Leu	Glu	Ala	Leu	Lys	Gly	Trp	Asp	Gln
			80					85						90

Gly	Leu	Lys	Gly	Met	Cys	Val	Gly	Glu	Lys	Arg	Lys	Ile	Thr	Ile
			95					100						105

Pro	Pro	Ala	Leu	Gly	Tyr	Gly	Lys	Glu	Gly	Lys	Gly	Lys	Ile	Pro
			110					115						120

Pro	Glu	Ser	Thr	Leu	Ile	Phe	Asn	Ile	Asp	Leu	Leu	Glu	Ile	Arg
			125					130						135

Asn	Gly	Pro	Arg	Ser	His	Glu	Ser	Phe	Gln	Glu	Met	Asp	Leu	Asn
			140					145						150

Asp	Asp	Trp	Lys	Leu	Ser	Lys	Asp	Glu	Val	Lys	Ala	Tyr	Leu	Lys
				155					160					165
Lys	Glu	Phe	Glu	Lys	His	Gly	Ala	Val	Val	Asn	Glu	Ser	His	His
				170					175					180
Asp	Ala	Leu	Val	Glu	Asp	Ile	Phe	Asp	Lys	Glu	Asp	Glu	Asp	Lys
				185					190					195
Asp	Gly	Phe	Ile	Ser	Ala	Arg	Glu	Phe	Thr	Tyr	Lys	His	Asp	Glu
				200					205					210

Leu

<210> 146
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 146
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<210> 147
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 147
 gccagagca ggaggaatga tgagc 25

<210> 148
 <211> 49
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 148
 gtggaacgag gtcttgactc tgttcgtcac ttctttgatt ggggctttg 49

<210> 149
 <211> 2196
 <212> DNA
 <213> Homo sapiens

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ctttgggagg ccaaggcggg tggattacct ccctctgttt agtagaaatg 2000
ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtggtgg 2050
cgtgtgctg taatccagc ttttgggag gctgaggcag gagaatcgt 2100
tgagcccggg aagcagaggt tgcagtgaac tgagatagt atagtgccac 2150
tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150

<211> 215

<212> PRT

<213> Homo sapiens

<400> 150

Met	His	Arg	Asp	Ala	Trp	Leu	Pro	Arg	Pro	Ala	Phe	Ser	Leu	Thr
1				5					10					15
Gly	Leu	Ser	Leu	Phe	Phe	Ser	Leu	Val	Pro	Pro	Gly	Arg	Ser	Met
			20						25					30
Glu	Val	Thr	Val	Pro	Ala	Thr	Leu	Asn	Val	Leu	Asn	Gly	Ser	Asp
				35					40					45
Arg	Arg	Leu	Val	Phe	Ala	Val	Asn	Leu	Val	Tyr	Thr	Val	Asn	His
				50					55					60
Lys	Gln	Phe	Ser	Leu	Asn	Trp	Thr	Tyr	Gln	Glu	Cys	Asn	Asn	Cys
				65					70					75
Ser	Glu	Glu	Met	Phe	Leu	Gln	Phe	Arg	Met	Lys	Ile	Ile	Asn	Leu
				80						85				90
Lys	Leu	Glu	Arg	Phe	Gln	Asp	Arg	Val	Glu	Phe	Ser	Gly	Asn	Pro
				95					100					105
Ser	Lys	Tyr	Asp	Val	Ser	Val	Met	Leu	Arg	Asn	Val	Gln	Pro	Glu

110	115	120
Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg		
125	130	135
His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu		
140	145	150
Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser		
155	160	165
Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val		
170	175	180
Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp		
185	190	195
Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro		
200	205	210
Asp Asp Gly Ala Lys		
215		

<110> 151
 <111> 524
 <112> DNA
 <113> Homo sapiens

<220>
 <221> unsure
 <222> 103, 233
 <223> unknown base

<400> 151
 gtgttatatg tectgaagta catccgtgca ttttttttag catccaacca 50
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 gcaactgcctt cagcctcacc gggctcagtc tctttttctc tttgggtgcca 200
 ccaggacgga gcatggagg' cctcagatgcc tgnacacacat caactctctc 250
 atgtgtctc atgagagact gcaatgcaat tcaactctctc ctacacactc 300
 ataa aca agtttctct gcaatgcaat tcaactctctc ctacacactc 350
 ctctgaggag atgtttctct agttctgcat gaagatcatt aaactdaacc 400
 tggagcgggtt tcaagatgcc gtggagttct cagggaacac cagcaagtac 450
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500
 caactgctac atcatqaacc cccc 524

<210> 152

<211> 368
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 56, 123
<223> unknown base

<400> 152
tcacgggggt catctctttt tctctttggt gccaccagg acggagcatg 50
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ccctgaactg gatttaccag gactgcaaca actggctctg aggagatggt 200
ccttcagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250
ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300
tcgggtgatg tgagaaacgt gcagccggag gatgagggga tttacaactg 350
ttacatcatg aattcccc 368

<210> 153
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 153
acggagcatg gaggtccaca gtac 24

<210> 154
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 154
tcgggtgatg tgagaaacgt gcagccggag 24

<210> 155
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 155

cgctgacct gcaccttcaa ctctgctac acagtgaacc acaaacagtt 50

<210> 156

<211> 2680

<212> DNA

<213> Homo sapiens

<400> 156

tggggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50

ggggtgctcc cggatggcct cctgttcttc ttgtgtgtgc taatgtgtgt 100

cggggaccca ggcctccggc cgggacgtca cccccagtg gtgctggctc 150

ctgggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagtg 200

gtgcactacc tctgtccaa gaagaccgaa agctacttca caatctggct 250

gaacctggaa ctgtgtgtgc ctgtcatcat tgactgtgtg attgacaata 300

tcaggctggt ttacaacaaa acatccaggg ccaccagtt tctgatggt 350

gtggatgtac gtgctcctgg ctttgggaag accttctcac tggagtctct 400

ggaccccagc aaaagcagcg tgggttcttc ttccacacac atgggtggga 450

gccttggtgg ctggggctac acacggggtg aggatgtccg aggggctccc 500

tatgaactgg gccgagcccc aaatgaaaac gggccctact tctggccct 550

ccgcgagatg atcgaggaga tgtaccagct gtatgggggc ccctggtgtc 600

tggttgcccc cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650

cagccgcagg cctggaagga caagtatata cgggccttcg tgtcaactgg 700

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cggcaggaca cagaagggtt agtggccttc atgctgctc ctgggtgtga 1000

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atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157

<211> 412

<212> PRT

<213> Homo Sapien

<400> 157

Met	Gly	Leu	His	Leu	Arg	Pro	Tyr	Arg	Val	Gly	Leu	Leu	Pro	Asp
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Gly	Leu	Leu	Phe	Leu	Leu	Leu	Leu	Met	Leu	Leu	Ala	Asp	Pro
				20				25					30

Ala	Leu	Pro	Ala	Gly	Arg	His	Pro	Pro	Val	Val	Leu	Val	Pro	Gly
				35					40					45

Asp	Leu	Gly	Asn	Gln	Leu	Glu	Ala	Lys	Leu	Asp	Lys	Pro	Thr	Val
				50					55					60

Val	His	Tyr	Leu	Cys	Ser	Lys	Lys	Thr	Glu	Ser	Tyr	Phe	Thr	Ile
				65					70					75

Trp	Leu	Asn	Leu	Glu	Leu	Leu	Leu	Pro	Val	Ile	Ile	Asp	Cys	Trp
				80					85					90

Ile	Asp	Asn	Ile	Arg	Leu	Val	Tyr	Asn	Lys	Thr	Ser	Arg	Ala	Thr
				95					100					105

Gln	Phe	Pro	Asp	Gly	Val	Asp	Val	Arg	Val	Pro	Gly	Phe	Gly	Lys
				110					115					120

Thr	Phe	Ser	Leu	Glu	Phe	Leu	Asp	Pro	Ser	Lys	Ser	Ser	Val	Gly
				125					130					135

Ser	Tyr	Phe	His	Thr	Met	Val	Glu	Ser	Leu	Val	Gly	Trp	Gly	Tyr
				140					145					150

Thr	Arg	Gly	Glu	Asp	Val	Arg	Gly	Ala	Pro	Tyr	Asp	Trp	Arg	Arg
				155					160					165

Ala	Pro	Asn	Glu	Asn	Gly	Pro	Tyr	Phe	Leu	Ala	Leu	Arg	Glu	Met
				170					175					180

Ile	Gln	Gln	Met	Tyr	Gln	Gln	Tyr	Gln	Gln	Ile	Val	Val	Leu	Val
				185					190					195

Ala	His	Ser	Met	Gly	Asn	Met	Tyr	Thr	Leu	Tyr	Phe	Leu	Gln	Arg
				200					205					210

Gln	Pro	Gln	Ala	Trp	Lys	Asp	Lys	Tyr	Ile	Arg	Ala	Phe	Val	Ser
				215					220					225

Leu	Gly	Ala	Pro	Trp	Gly	Gly	Val	Ala	Lys	Thr	Leu	Arg	Val	Leu
				230					235					240

Ala	Ser	Gly	Asp	Asn	Asn	Arg	Ile	Pro	Val	Ile	Gly	Pro	Leu	Lys
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

245	250	255
Ile Arg Glu Gln Gln Arg Ser Ala Val Ser Thr Ser Trp Leu Leu		
260	265	270
Pro Tyr Asn Tyr Thr Trp Ser Pro Glu Lys Val Phe Val Gln Thr		
275	280	285
Pro Thr Ile Asn Tyr Thr Leu Arg Asp Tyr Arg Lys Phe Phe Gln		
290	295	300
Asp Ile Gly Phe Glu Asp Gly Trp Leu Met Arg Gln Asp Thr Glu		
305	310	315
Gly Leu Val Glu Ala Thr Met Pro Pro Gly Val Gln Leu His Cys		
320	325	330
Leu Tyr Gly Thr Gly Val Pro Thr Pro Asp Ser Phe Tyr Tyr Glu		
335	340	345
Ser Phe Pro Asp Arg Asp Pro Lys Ile Cys Phe Gly Asp Gly Asp		
350	355	360
Gly Thr Val Asn Leu Lys Ser Ala Leu Gln Cys Gln Ala Trp Gln		
365	370	375
Ser Arg Gln Glu His Gln Val Leu Leu Gln Glu Leu Pro Gly Ser		
380	385	390
Glu His Ile Glu Met Leu Ala Asn Ala Thr Thr Leu Ala Tyr Leu		
395	400	405
Lys Arg Val Leu Leu Gly Pro		
410		

<210> 158
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 158
 aggggata atattggtg aggtt

<210> 159
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 159
 ggtgccgctg cagaaagtag agcg 24

<210> 160
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 160
gccccaaatg aaaacgggccc ctacttcctg gccctccgcg agatg 45

<210> 161
<211> 1512
<212> DNA
<213> Homo sapiens

<400> 161
cgagcgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgcg 50
atggagagcg gggcctacgg cgcggccaag gcggggcggt ccttcgacct 100
gaggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150
tcttcgcctt gatcgtgttc tctgcctct atggtgaggg ctacagcaat 200
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accgaagga cgtgctggtg ggggcagact ctgtgagggc agccatcacc 500
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gacaaactacc aacagccatc ctccacccac aacggcggga ccacgaggg 700
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cagagagggc cctccccctt gccctggaat tcccatcag cctcctggaa 800
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 tctcattcaa ag 1512

<210> 162

<211> 224

<212> PRT

<213> Homo sapiens

<400> 162

Met	Glu	Ser	Gly	Ala	Tyr	Gly	Ala	Ala	Lys	Ala	Gly	Gly	Ser	Phe
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Asp	Leu	Arg	Arg	Phe	Leu	Thr	Gln	Pro	Gln	Val	Val	Ala	Arg	Ala
				20					25					30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly
				35					40					45

Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val
				50					55					60

Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly
				65					70					75

Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala
				80					85					90

Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Ile	Asp	Arg	Gly	Tyr	Leu	Val
				95					100					105

Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe
				110					115					120

Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro
				125					130					135

Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr
				140					145					150

Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly Val Leu Ala Ser Leu
155 160 165

Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp Phe Ile Gln Asn
170 175 180

Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr Ala Ser Tyr
185 190 195

Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe Thr Gln
200 205 210

Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
215 220

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164

gtgtactgag cggcgggtag 20

<210> 165

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 165

ctgaagggtga tggtgccct cac 23

<210> 166

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 166

ccaggaggct catgggaaag tcc 23

<210> 167

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 167

ncacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168

<211> 3143

<212> DNA

<213> Homo sapiens

<400> 168

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<210> 169
 <211> 802
 <212> PRT
 <213> Homo sapiens

<400> 169
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 35 40 45
 Pro Leu Phe Val Leu Ala Leu Leu Val Leu Ala Ser Ala Gly
 50 55 60
 Val Leu Leu Trp Tyr Phe Leu Gly Tyr Lys Ala Glu Val Met Val
 65 70 75
 Ser Gln Val Tyr Ser Gly Ser Leu Arg Val Leu Asn Arg His Phe
 80 85 90
 Ser Gln Asp Leu Thr Arg Arg Glu Ser Ser Ala Phe Arg Ser Glu

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Thr Ala Lys Ala Gln Lys Met Leu Lys	Glu Leu Ile Thr Ser Thr		
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Arg Leu Gly Thr Tyr Tyr Asn Ser Ser	Ser Val Tyr Ser Phe Gly		
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Glu Gly Pro Leu Thr Cys Phe Phe Trp	Phe Ile Leu Gln Ile Pro		
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Glu His Arg Arg Leu Met Leu Ser Pro	Glu Val Val Gln Ala Leu		
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Leu Val Glu Glu Leu Leu Ser Thr Val	Asn Ser Ser Ala Ala Val		
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Pro Tyr Arg Ala Glu Tyr Glu Val Asp	Pro Glu Gly Leu Val Ile		
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Leu Glu Ala Ser Val Lys Asp Ile Ala	Ala Leu Asn Ser Thr Leu		
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Gly Cys Tyr Arg Tyr Ser Tyr Val Gly	Gln Gly Gln Val Leu Arg		
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Leu Lys Gly Pro Asp His Leu Ala Ser	Ser Cys Leu Trp His Leu		
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Gln Gly Pro Lys Asp Leu Met Leu Lys	Leu Arg Leu Glu Trp Thr		
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Leu Ala Glu Cys Arg Asp Arg Leu Ala	Met Tyr Asp Val Ala Gly		
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Pro Leu Glu Lys Arg Leu Ile Thr Ser	Val Tyr Gly Cys Ser Arg		
275	280	285	
Gln Glu Pro Val Val Glu Val Leu Ala	Ser Gly Ala Ile Met Ala		
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Val Val Trp Lys Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe Val		
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Thr Leu Asp Asn Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr Pro		
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Tyr Phe Pro Ser Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp His		
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Ala Tyr Ala Leu Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr Gln		

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Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile
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Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly
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Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly
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Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro
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Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys
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Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys
	470	475	480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile
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Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly
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Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe
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Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro
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Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu
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His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly
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Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu
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Gln Val Arg Gly	Arg His Ile Cys Gly	Gly Ala Leu Ile Ala	Asp
	590	595	600
Arg Trp Val Ile	Thr Ala Ala His Cys	Phe Ser Val Asp Ser	Met
	605	610	615
Ala Ser Thr Val	Leu Trp Thr Val Phe	Leu Gly Lys Val Trp	Gln
	620	625	630
Asn Ser Arg Trp	Pro Gly Glu Val Ser	Phe Lys Val Ser Arg	Leu
	635	640	645
Leu Leu His Pro	Tyr His Glu Glu Asp	Ser His Asp Tyr Asp	Val
	650	655	660
Ala Leu Leu Gln	Leu Asp His Pro Val	Val Arg Ser Ala Ala	Val

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Arg Pro Val Cys Leu Pro Ala Arg Ser	His Phe Phe Glu Pro Gly	
680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly	Ala Leu Arg Glu Gly Gly	
695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val	Asp Val Gln Leu Ile Pro	
710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg	Tyr Gln Val Thr Pro Arg	
725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly	Lys Lys Asp Ala Cys Gln	
740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys	Lys Ala Leu Ser Gly Arg	
755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp	Gly Leu Gly Cys Gly Arg	
770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg	Ile Thr Gly Val Ile Ser	
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Trp Ile Gln Gln Val Val Thr		
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<211> 1327

<212> DNA

<213> Homo sapiens

<400> 170

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<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taatccagca gtgcagggcg gg 24

<210> 172

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 172

taatccagca gtgcagggcg gg 22

<210> 173

<211> 50

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 173

atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 174

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<210> 175

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 175

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<210> 176

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 176

aggtatgattt gcggtgcacc caggggcagt ggacgatcca gaacaggagg 50

<210> 177

<211> 1510

<212> DNA

<213> Homo sapiens

<400> 177

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<210> 178
 <211> 354
 <212> PRT
 <213> Homo sapiens

<400> 178

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Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30
Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45
Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60
His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75
Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90
Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105
Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120
Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135
Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150
Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Ile	Gly	Asn	Val	His	Leu
				155					160					165
Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180
Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195
Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210
Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225
Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Arg
				230					235					240
Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285

Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
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Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
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<210> 179

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 179

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<210> 180

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 180

gctattacaa cggttcttgc ggcagc 26

<210> 181

<211> 44

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 181

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<210> 182

<211> 3240

<212> DNA

<213> Homo sapiens

<400> 182

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<210> 183

<211> 713

<212> PRT

<213> Homo sapiens

<400> 183

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Pro	Pro	Ala	Val	Leu	Glu	Val	Gln	Gly	Thr	Leu	Gln	Arg	Pro	35	40	45		
Leu	Val	Arg	Asp	Ser	Arg	Thr	Ser	Pro	Ala	Asn	Cys	Thr	Trp	Leu	50	55	60	
Ile	Leu	Gly	Ser	Lys	Glu	Gln	Thr	Val	Thr	Ile	Arg	Phe	Gln	Lys	65	70	75	
Leu	His	Leu	Ala	Cys	Gly	Ser	Glu	Arg	Leu	Thr	Leu	Arg	Ser	Pro	80	85	90	
Leu	Gln	Pro	Leu	Ile	Ser	Leu	Cys	Glu	Ala	Pro	Pro	Ser	Pro	Leu	95	100	105	
Gln	Leu	Pro	Gly	Gly	Asn	Val	Thr	Ile	Thr	Tyr	Ser	Tyr	Ala	Gly	110	115	120	
Ala	Arg	Ala	Pro	Met	Gly	Gln	Gly	Phe	Leu	Leu	Ser	Tyr	Ser	Gln	125	130	135	
Asp	Trp	Leu	Met	Cys	Leu	Gln	Glu	Glu	Phe	Gln	Cys	Leu	Asn	His	140	145	150	
Arg	Cys	Val	Ser	Ala	Val	Gln	Arg	Cys	Asp	Gly	Val	Asp	Ala	Cys	155	160	165	
Gly	Asp	Gly	Ser	Asp	Gln	Ala	Gly	Cys	Ser	Ser	Asp	Pro	Phe	Pro	170	175	180	
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr				

185										190					195				
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His					
				200						205				210					
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp					
				215					220					225					
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp					
				230					235					240					
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro					
				245					250					255					
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn					
				260					265					270					
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val					
				275					280					285					
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala					
				290					295					300					
Ile	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys					
				305					310					315					
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg					
				320					325					330					
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala					
				335					340					345					
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His					
				350					355					360					
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr					
				365					370					375					
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly					
				380					385					390					
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg					
				395					400					405					
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly					
				410					415					420					
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr					
				425					430					435					
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu					
				440					445					450					
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys					
				455					460					465					
Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu					

470	475	480
Ser Arg Met Glu Ala Glu Ile Val Gln Gln Gln Ala Pro Pro Ser		
485	490	495
Tyr Gly Gln Leu Ile Ala Gln Gly Ala Ile Pro Pro Val Glu Asp		
500	505	510
Phe Pro Thr Glu Asn Pro Asn Asp Asn Ser Val Leu Gly Asn Leu		
515	520	525
Arg Ser Leu Leu Gln Ile Leu Arg Gln Asp Met Thr Pro Gly Gly		
530	535	540
Gly Pro Gly Ala Arg Arg Arg Gln Arg Gly Arg Leu Met Arg Arg		
545	550	555
Leu Val Arg Arg Leu Arg Arg Trp Gly Leu Leu Pro Arg Thr Asn		
560	565	570
Thr Pro Ala Arg Ala Ser Glu Ala Arg Ser Gln Val Thr Pro Ser		
575	580	585
Ala Ala Pro Leu Glu Ala Leu Asp Gly Gly Thr Gly Pro Ala Arg		
590	595	600
Glu Gly Gly Ala Val Gly Gly Gln Asp Gly Glu Gln Ala Pro Pro		
605	610	615
Leu Pro Ile Lys Ala Pro Leu Pro Ser Ala Ser Thr Ser Pro Ala		
620	625	630
Pro Thr Thr Val Pro Glu Ala Pro Gly Pro Leu Pro Ser Leu Pro		
635	640	645
Leu Glu Pro Ser Leu Leu Ser Gly Val Val Gln Ala Leu Arg Gly		
650	655	660
Arg Leu Leu Pro Ser Leu Gly Pro Pro Gly Pro Thr Arg Ser Pro		
665	670	675
Pro Gly Pro His Thr Ala Val Leu Ala Leu Glu Asp Glu Asp Asp		
680	685	690
Val Leu Leu Val Pro Leu Ala Glu Pro Gly Val Trp Val Ala Glu		
695	700	705
Ala Glu Asp Glu Pro Leu Leu Thr		
710		

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184
ggctgtcact gtggagacac 20

<210> 185
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 185
gcaaggtcat tacagctg 18

<210> 186
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 186
agaacatagg agcagtcacca etc 23

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 187
tgctgtgtgc tgcacaatct cag 23

<210> 188
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 188
ggctattgct tgccttggga cagaccctgt ggcttaggt ctggc 45

<210> 189
<211> 663
<212> DNA
<213> Homo sapiens

<400> 189
cgagctgggc gagaagtagg ggagggcggg gctccggcgc ggtggcggtt 50
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100

gaaagtgtctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150
 aataaaacat cgccccttct gcttcagtgt gaaaggccac gtgaagatgc 200
 tgccggtggc actaactgtg acatctatga ccttttttat catcgacaaa 250
 gccctgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300
 atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350
 tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400
 atgctcatcg tatctgtgtt ggcaactgata ccagaaacca caacattgac 450
 agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500
 acggggccct tatttaccgg aagcttctgt tcaatcccag cggctcttac 550
 cagaaaaagc ctgtgcatga aaaaaagaa gttttgtaat tttatattac 600
 tttttagttt gatactaagt attaaacata ttctgtatt cttccaaaaa 650
 aaaaaaaaaa aaa 662

<210> 190
 <211> 152
 <212> PRT
 <213> Homo sapiens

<400> 190
 Met Asp Asn Val Gln Pro Lys Ile Lys His Arg Pro Phe Cys Phe
 1 5 10 15
 Ser Val Lys Gly His Val Lys Met Leu Arg Leu Ala Leu Thr Val
 20 25 30
 Thr Ser Met Thr Phe Phe Ile Ile Ala Gln Ala Pro Glu Pro Tyr
 35 40 45
 Ile Val Ile Thr Gly Phe Glu Val Thr Val Ile Leu Phe Phe Ile
 50 55 60
 Leu Leu Tyr Val Leu Thr Ile Asp Arg Leu Met Lys Trp Leu Phe
 65 70 75
 Trp Pro Leu Leu Asp Ile Ile Asn Ser Leu Val Thr Thr Val Ile
 80 85 90
 Met Leu Ile Val Ser Val Leu Ala Leu Ile Pro Glu Thr Thr Thr
 95 100 105
 Leu Thr Val Gly Gly Gly Val Phe Ala Leu Val Thr Ala Val Cys
 110 115 120
 Cys Leu Ala Asp Gly Ala Leu Ile Tyr Arg Lys Leu Leu Phe Asn
 125 130 135

Pro Ser Gly Pro Tyr Gln Lys Lys Pro Val His Glu Lys Lys Glu
 140 145 150

Val Leu

<210> 191
 <211> 495
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 78, 212, 234, 487
 <223> unknown base

<400> 191
 gggcgagaag taggggaggg cgtgttcgc gcgggtggcg gttgctatcg 50
 ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100
 tgggtgctgg gtctgcagac gogatggata acgtgcagcc gaaaataaaa 150
 catcgccctt tctgcttcag tgtgaaaggg cactgaaga tgctgoggt 200
 ggcactaact gngacatcta tgacottttt tatnategca caagcccttg 250
 aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300
 atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350
 gacttttgctt gatattatca actcactggg aacaacagta ttcattgtca 400
 tcttatctgt gttggcactg ataccagaaa ccacaacatt gacagttggt 450
 ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 192
 cgttttgcag aacctactca ggcag 25

<210> 193
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 193

cctccaccaa ctgtcaatgt tgtgg 25

<210> 194

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 194

aaagtgtctg tgctgggtct gcagacgca tggataacgt 40

<210> 195

<211> 1879

<212> DNA

<213> Homo sapien

<400> 195

cagccccg cgccggccga gtcgtgagc cgcggtgcc ggacgggacg 50
ggatgggcta ggctgggcgc gcccccggg ccccgccgtg ggcattggcg 100
caatggcccc ggctgtctg ctgctctgc tggcccagt gctcctggc 150
ggcgccccg agctggcccc cgcgccttc acgtgcccc tccgggtggc 200
cgcgccacg aaccgcgtag ttgcgccac ccggggacc gggacccctg 250
ccgagcgca cgcgcacggc ttggcgctcg cctggagcc tgcctggcg 300
tcccccgcg ggcccgccaa cttcttggc atggtagaca acctgcaggg 350
ggactctggc cgcggtact acctggagat gctgatcggg accccccgc 400
agaagctaca gattctcgtt gacactggaa gcagtaactt tgccgtggca 450
ggaacccgc actcctacat agacacgtac ttgacacag agaggtctag 500
cagataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550
actggacggg cttcgttggg gaagacctcg tcacatccc caaaqgcttc 600
aatacttctt ttcttgtaaa cattgcaact attttgact cagagaa 650
ctttttgcct gggattaaat ggaatggaat acctggccta gcttatgcca 700
caattgcaaa gccatcaagt tctctggaga ccttcttga ctccctggtg 750
acacaagcaa acatcccaaa cgtttttctc atgcagatgt gtggagccgg 800
cttccccgtt cctggatctg ggaaccaagg aggtagtctt gtcttgggtg 850
gaattgaacc aagtttgtat aaaggagaaa tctgggtata cctattaag 900
gaagagtggc actaccagat agaaattctg aaattggaaa ttggaggcca 950

aagccttaal ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000
acagtggcac cacgctgctg cgcccgcccc agaaggtgtt tgatgcggtg 1050
gtggaagctg tggcccgcg c atctctgatt ccagaattct ctgatggttt 1100
ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttgg 1150
cttacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200
tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250
ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300
atgcgctggg gatcgggtgc acggtgatgg agggcttcta cgtcatcttc 1350
gacagagccc agaagagggg gggcttcgca gcgagccct gtgcagaaat 1400
tgcaggtgct gcagtgtctg aaatttccgg gcctttctca acagaggatg 1450
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acatttccag ggcagcagcc gggatcgatg gtggcgctt ctctgtgcc 1750
caccgtctt caatctctgt tctgtccca gatgccttct agattcactg 1800
tcttttgatt ctgattttc aagctttcaa atcctcccta ctccaagaa 1850
aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT

<213> Homo sapien

<400> 196

Met Gly Ala Leu Ala Arg Ala Leu Leu Leu Pro Leu Leu Ala Gln
1 5 10 15

Trp Leu Leu Arg Ala Ala Pro Glu Leu Ala Pro Ala Pro Phe Thr
20 25 30

Leu Pro Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro
35 40 45

Thr Pro Gly Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu
50 55 60

Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala		65	70	75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg		80	85	90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu		95	100	105
Gln	Ile	Leu	Val	Asp	Thr	Gly	Ser	Ser	Asn	Phe	Ala	Val	Ala	Gly		110	115	120
Thr	Pro	His	Ser	Tyr	Ile	Asp	Thr	Tyr	Phe	Asp	Thr	Glu	Arg	Ser		125	130	135
Ser	Thr	Tyr	Arg	Ser	Lys	Gly	Phe	Asp	Val	Thr	Val	Lys	Tyr	Thr		140	145	150
Gln	Gly	Ser	Trp	Thr	Gly	Phe	Val	Gly	Glu	Asp	Leu	Val	Thr	Ile		155	160	165
Pro	Lys	Gly	Phe	Asn	Thr	Ser	Phe	Leu	Val	Asn	Ile	Ala	Thr	Ile		170	175	180
Phe	Glu	Ser	Glu	Asn	Phe	Phe	Leu	Pro	Gly	Ile	Lys	Trp	Asn	Gly		185	190	195
Ile	Leu	Gly	Leu	Ala	Tyr	Ala	Thr	Leu	Ala	Lys	Pro	Ser	Ser	Ser		200	205	210
Leu	Glu	Thr	Phe	Phe	Asp	Ser	Leu	Val	Thr	Gln	Ala	Asn	Ile	Pro		215	220	225
Asn	Val	Phe	Ser	Met	Gln	Met	Cys	Gly	Ala	Gly	Leu	Pro	Val	Ala		230	235	240
Gly	Ser	Gly	Thr	Asn	Gly	Gly	Ser	Leu	Val	Leu	Gly	Gly	Ile	Glu		245	250	255
Pro	Ser	Leu	Tyr	Lys	Gly	Asp	Ile	Trp	Tyr	Thr	Pro	Ile	Lys	Glu		260	265	270
Glu	Trp	Tyr	Tyr	Gln	Ile	Glu	Ile	Leu	Lys	Leu	Glu	Ile	Gly	Gly		275	280	285
Gln	Ser	Leu	Asn	Leu	Asp	Cys	Arg	Gln	Thr	Asn	Ala	Asp	Lys	Ala		290	295	300
Ile	Val	Asp	Ser	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gln	Lys	Val		305	310	315
Phe	Asp	Ala	Val	Val	Glu	Ala	Val	Ala	Arg	Ala	Ser	Leu	Ile	Pro		320	325	330
Glu	Phe	Ser	Asp	Gly	Phe	Trp	Thr	Gly	Ser	Gln	Leu	Ala	Cys	Trp		335	340	345

Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
350	355	360	
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
365	370	375	
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
380	385	390	
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu
395	400	405	
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp
410	415	420	
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu
425	430	435	
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr
440	445	450	
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu
455	460	465	
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly
470	475	480	
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg
485	490	495	
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser
500	505	510	
Ser Leu Val Arg	His Arg Trp Lys		
515			

<210> 197

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 197

ggagaagat accgattt 21

<210> 198

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 198

ggaaaattgga ggccaaagc 19

<210> 199
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 199
ggatgtagcc agcaactgtg 20

<210> 200
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 200
gacttgacct gttctcttc 19

<210> 201
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 201
ggctcctgtgc ctggatgg 18

<210> 202
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 202
gaagacacac cttctcttc 22

<210> 203
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 203
tgatgacacag ttcagcacct gttg 24

<210> 204

<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 204
cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205
<211> 1939
<212> DNA
<213> Homo sapiens

<400> 205
cgccctccgcc ttccgaggct gacgcgcccg ggccgccgttc caggcctgtg 50
cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100
ggggcgggagc cgggagggcg ggccggcatg gaggcgctgc tgcctgggcgc 150
ggggctgctg ctgggcgctt acgtgcttgc ctactacaac ctggtgaagg 200
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atggccttgg acttggcag tctggcctcg gtgcgggctt ttgccactgc 450
ctttctgagc tctgagccac ggttgacat cctcatccac aatgccggta 500
tcagttcctg tggccggacc cgtgaggcgt ttaacctgct gcttcgggtg 550
aaccatatcg gtccctttct gctgacacat ctgctcctgc cttgcctgaa 600
ggcatatgac cctagccgcg tgggtggtgg agcctcagct gcccaactgc 650
ggggaggtct tgaattcaaa cgcctggacc gcccaatggt gggctggcgg 700
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gaggetggca gggcttgggc ctggggagga tgctgaaccc gatgaagacc 1100
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 tctcggaat ttggatgtag tattttcagg cccaccctt attgattctg 1550
 atcagctctg gacgagagc agggagtttg caatgtgatg cactgccaac 1600
 attgagaatt agtgaactga tcttttcca accgtctagc taggtagtta 1650
 aattaccccc atgttaatga agcgaatta ggctcccgag ctaagggact 1700
 cgctagggt ctcacagtga gtaggaggag ggctgggat ctgaacccaa 1750
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 cagggcaggg cagctggtat cgaggtgcc catgggagta aggggacgcc 1850
 ttccggggcg atgcagggct ggggtcatct gtatctgaag cccctcgaa 1900
 taaagcgctg tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206

<211> 377

<212> PRT

<213> Homo sapiens

<400> 206

Met Glu Ala Ile Leu Leu Gly Ala Glu Leu Leu Gly Ala Tyr
 1 5 10

Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Lys Gly Gly
 20 25 30

Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn
 35 40 45

Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly
 50 55 60

Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala
 65 70 75

Ala Ala Phe Asp	Leu Arg Gln Glu Ser	Gly Asn Asn Glu Val	Ile
	80	85	90
Phe Met Ala Leu Asp	Leu Ala Ser Leu	Ala Ser Val Arg Ala	Phe
	95	100	105
Ala Thr Ala Phe	Leu Ser Ser Glu Pro	Arg Leu Asp Ile Leu	Ile
	110	115	120
His Asn Ala Gly	Ile Ser Ser Cys Gly	Arg Thr Arg Glu Ala	Phe
	125	130	135
Asn Leu Leu Leu	Arg Val Asn His Ile	Gly Pro Phe Leu Leu	Thr
	140	145	150
His Leu Leu Leu	Pro Cys Leu Lys Ala	Cys Ala Pro Ser Arg	Val
	155	160	165
Val Val Val Ala	Ser Ala Ala His Cys	Arg Gly Arg Leu Asp	Phe
	170	175	180
Lys Arg Leu Asp	Arg Pro Val Val Gly	Trp Arg Gln Glu Leu	Arg
	185	190	195
Ala Tyr Ala Asp	Thr Lys Leu Ala Asn	Val Leu Phe Ala Arg	Glu
	200	205	210
Leu Ala Asn Gln	Leu Glu Ala Thr Gly	Val Thr Cys Tyr Ala	Ala
	215	220	225
His Pro Gly Pro	Val Asn Ser Glu Leu	Phe Leu Arg His Val	Pro
	230	235	240
Gly Trp Leu Arg	Pro Leu Leu Arg Pro	Leu Ala Trp Leu Val	Leu
	245	250	255
Arg Ala Pro Arg	Gly Gly Ala Gln Thr	Pro Leu Tyr Cys Ala	Leu
	260	265	270
Gln Glu Gly Ile	Glu Pro Leu Ser Gly	Arg Tyr Phe Ala Asn	Cys
	275	280	285
His Val Glu Glu	Val Pro Pro Ala Ala	Arg Asp Asp Arg Ala	Ala
	290	295	300
His Arg Leu Trp	Glu Ala Ser Lys Arg	Leu Ala Gly Leu Gly	Pro
	305	310	315
Gly Glu Asp Ala	Glu Pro Asp Glu Asp	Pro Gln Ser Glu Asp	Ser
	320	325	330
Glu Ala Pro Ser	Ser Leu Ser Thr Pro	His Pro Glu Glu Pro	Thr
	335	340	345
Val Ser Gln Pro	Tyr Pro Ser Pro Gln	Ser Ser Pro Asp Leu	Ser
	350	355	360

Lys Met Thr His Arg Ile Gln Ala Lys Val Glu Pro Glu Ile Gln
 365 370 375

Leu Ser

<210> 207
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 207
 attcatggcc ttggacttgg ccag 24

<210> 208
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 208
 aggcacgtgg cctcaagctg gttg 24

<210> 209
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 209
 attctcgcgc tctgacccac ggttggacat cctcatccac aatgc 45

<210> 210
 <211> 3716
 <212> DNA
 <213> Homo sapiens

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<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

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			20					25						30
Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
			35					40						45
Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
			50					55						60
Leu	Pro	Asp	Gly	Thr	Ile	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
			65					70						75
His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
			80					85						90
Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
			95					100						105
Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
			110					115						120
Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
			125					130						135

Cys Gly Pro Pro	Trp Gly His Pro Glu	Pro Thr Val Ser Trp Trp	140	145	150
Lys Asp Gly Lys	Pro Leu Ala Leu Gln	Pro Gly Arg His Thr Val	155	160	165
Ser Gly Gly Ser	Leu Leu Met Ala Arg	Ala Glu Lys Ser Asp Glu	170	175	180
Gly Thr Tyr Met	Cys Val Ala Thr Asn	Ser Ala Gly His Arg Glu	185	190	195
Ser Arg Ala Ala	Arg Val Ser Ile Gln	Glu Pro Gln Asp Tyr Thr	200	205	210
Glu Pro Val Glu	Leu Leu Ala Val Arg	Ile Gln Leu Glu Asn Val	215	220	225
Thr Leu Leu Asn	Pro Asp Pro Ala Glu	Gly Pro Lys Pro Arg Pro	230	235	240
Ala Val Trp Leu	Ser Trp Lys Val Ser	Gly Pro Ala Ala Pro Ala	245	250	255
Gln Ser Tyr Thr	Ala Leu Phe Arg Thr	Gln Thr Ala Pro Gly Gly	260	265	270
Gln Gly Ala Pro	Trp Ala Glu Glu Leu	Leu Ala Gly Trp Gln Ser	275	280	285
Ala Glu Leu Gly	Gly Leu His Trp Gly	Gln Asp Tyr Glu Phe Lys	290	295	300
Val Arg Pro Ser	Ser Gly Arg Ala Arg	Gly Pro Asp Ser Asn Val	305	310	315
Leu Leu Leu Arg	Leu Pro Glu Lys Val	Pro Ser Ala Pro Pro Gln	320	325	330
Glu Val Thr Leu	Lys Pro Gly Asn Gly	Thr Val Phe Val Ser Trp	335	340	345
Val Pro Pro Pro	Ala Glu Asn His Asn	Gly Ile Ile Arg Gly Tyr	350	355	360
Gln Val Trp Ser	Leu Gly Asn Thr Ser	Leu Phe Phe Ala Asn Trp	365	370	375
Thr Val Val Gly	Glu Gln Thr Gln Leu	Glu Ile Ala Thr His Met	380	385	390
Pro Gly Ser Tyr	Cys Val Gln Val Ala	Ala Val Thr Gly Ala Gly	395	400	405
Ala Gly Glu Pro	Ser Arg Pro Val Cys	Leu Leu Leu Glu Gln Ala	410	415	420

Met Glu Arg Ala Thr Gln Glu Pro Ser	Glu His Gly Pro Trp Thr
425	430 435
Leu Glu Gln Leu Arg Ala Thr Leu Lys	Arg Pro Glu Val Ile Ala
440	445 450
Thr Cys Gly Val Ala Leu Trp Leu Leu	Leu Leu Gly Thr Ala Val
455	460 465
Cys Ile His Arg Arg Arg Arg Ala Arg	Val His Leu Gly Pro Gly
470	475 480
Leu Tyr Arg Tyr Thr Ser Glu Asp Ala	Ile Leu Lys His Arg Met
485	490 495
Asp His Ser Asp Ser Gln Trp Leu Ala	Asp Thr Trp Arg Ser Thr
500	505 510
Ser Gly Ser Arg Asp Leu Ser Ser Ser	Ser Ser Leu Ser Ser Arg
515	520 525
Leu Gly Ala Asp Ala Arg Asp Pro Leu	Asp Cys Arg Arg Ser Leu
530	535 540
Leu Ser Trp Asp Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro Asp
545	550 555
Thr Ser Thr Phe Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser Ser
560	565 570
Thr Pro Ala Arg Pro Ser Pro Gln Val	Pro Ala Val Arg Arg Leu
575	580 585
Pro Pro Gln Leu Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser Asp
590	595 600
Ser Leu Cys Ser Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser Leu
605	610 615
Ala Pro Ala Glu Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu Gln
620	625 630
His Ala Thr Ser Ser Pro Leu Leu Arg	Gly Ser His Ser Leu Glu
635	640 645
Leu Arg Ala Cys Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu Ser
650	655 660
Gln Ser Pro Gly Ala Val Pro Gln Ala	Leu Val Ala Trp Arg Ala
665	670 675
Leu Gly Pro Lys Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr Arg
680	685 690
His Leu Pro Pro Ala Pro Leu Phe Pro	His Glu Thr Pro Pro Thr
695	700 705

Gln Ser Gln Gln Thr Gln Pro Pro Val Ala Pro Gln Ala Pro Ser	710	715	720
Ser Ile Leu Leu Pro Ala Ala Pro Ile Pro Ile Leu Ser Pro Cys	725	730	735
Ser Pro Pro Ser Pro Gln Ala Ser Ser Leu Ser Gly Pro Ser Pro	740	745	750
Ala Ser Ser Arg Leu Ser Ser Ser Ser Leu Ser Ser Leu Gly Glu	755	760	765
Asp Gln Asp Ser Val Leu Thr Pro Glu Glu Val Ala Leu Cys Leu	770	775	780
Glu Leu Ser Glu Gly Glu Glu Thr Pro Arg Asn Ser Val Ser Pro	785	790	795
Met Pro Arg Ala Pro Ser Pro Pro Thr Thr Tyr Gly Tyr Ile Ser	800	805	810
Val Pro Thr Ala Ser Glu Phe Thr Asp Met Gly Arg Thr Gly Gly	815	820	825
Gly Val Gly Pro Lys Gly Gly Val Leu Leu Cys Pro Pro Arg Pro	830	835	840
Cys Leu Thr Pro Thr Pro Ser Glu Gly Ser Leu Ala Asn Gly Trp	845	850	855
Gly Ser Ala Ser Glu Asp Asn Ala Ala Ser Ala Arg Ala Ser Leu	860	865	870
Val Ser Ser Ser Asp Gly Ser Phe Leu Ala Asp Ala His Phe Ala	875	880	885
Arg Ala Leu Ala Val Ala Val Asp Ser Phe Gly Phe Gly Leu Glu	890	895	900
Pro Arg Glu Ala Asp Cys Val Phe Ile Asp Ala Ser Ser Pro Pro	905	910	915
Ser Pro Arg Asp Glu Ile Phe Leu Thr Pro Asn Leu Ser Leu Pro	920	925	930
Leu Trp Glu Trp Arg Pro Asp Trp Leu Glu Asp Met Glu Val Ser	935	940	945
His Thr Gln Arg Leu Gly Arg Gly Met Pro Pro Trp Pro Pro Asp	950	955	960
Ser Gln Ile Ser Ser Gln Arg Ser Gln Leu His Cys Arg Met Pro	965	970	975
Lys Ala Gly Ala Ser Pro Val Asp Tyr Ser	980	985	

<210> 212
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 212
gaagggaacct acatgtgtgt ggcc 24

<210> 213
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 213
actgaccttc cagctgagcc acac 24

<210> 214
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 214
aggactaac ggagcctgtg gagcttcttg ctgtgcgaat tcagctggaa 50

<210> 215
<211> 2749
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 1869, 1887
<223> unknown base

<400> 215
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gggggttcga agggggaact gtgtccctgc agtgcacctc cagggaagag 150
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tgggtgtctt ggcaacatct atgcagaaga agaaggccac gacacaaatga 250
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<210> 216

<211> 332

<212> FRT

<213> HOMO SAPIENS

<400> 216

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Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly
				20				25					30	

Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp
				35				40					45	

His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50										55					60				
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met					
				65						70				75					
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu					
				80					85					90					
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr					
				95					100					105					
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile					
				110					115					120					
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser					
				125					130					135					
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala					
				140					145					150					
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu					
				155					160					165					
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu					
				170					175					180					
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr					
				185					190					195					
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro					
				200					205					210					
Ala	Gly	Ser	Ser	Arg	Pro	Pro	Met	Gln	Leu	Asp	Ser	Thr	Ser	Ala					
				215					220					225					
Glu	Asp	Thr	Ser	Pro	Ala	Leu	Ser	Ser	Gly	Ser	Ser	Lys	Pro	Arg					
				230					235					240					
Val	Ser	Ile	Pro	Met	Val	Arg	Ile	Leu	Ala	Pro	Val	Leu	Val	Leu					
				245					250					255					
Leu	Ser	Leu	Leu	Ser	Ala	Ala	Gly	Leu	Ile	Ala	Phe	Cys	Ser	His					
				260					265					270					
Leu	Leu	Leu	Trp	Arg	Lys	Glu	Ala	Gln	Gln	Ala	Thr	Glu	Thr	Ile					
				275					280					285					
Arg	Asn	Glu	Lys	Phe	Trp	Leu	Ser	Arg	Leu	Thr	Ala	Glu	Glu	Lys					
				290					295					300					
Glu	Ala	Pro	Ser	Gln	Ala	Pro	Glu	Gly	Asp	Val	Ile	Ser	Met	Pro					
				305					310					315					
Pro	Leu	His	Thr	Ser	Glu	Glu	Glu	Leu	Gly	Phe	Ser	Lys	Phe	Val					
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Ser	Ala																		

<210> 217
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 217
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<210> 218
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 218
 cgtcttccccc ctgcttggtg gtgg 24

<210> 219
<211> 47
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 219
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<210> 220
<211> 950
<212> DNA
<213> Homo sapiens

<400> 220
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 ttgtgactaa ggggggggac cccagaggaag acagcccaga aacagggtgga 150
 ttgtgactaa ggggggggac cccagaggaag acagcccaga aacagggtgga 200
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 ctccagttag gccaaactct acggtcgttg tgaactggcc agagtgtac 500
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 tgcccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650
 ggtgcagcaa cctcaccctg aacgtcccca acgtgtgccg gatgtactgc 700
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850
 gatggacgga accatgcaca gcaggtggg aaatgtgggt tggttcctga 900
 cctaggcttg ggaagacaag ccagcgaata aaggatgggt gaacgtgaaa 950

<210> 221

<211> 146

<212> PRT

<213> Homo sapiens

<400> 221

Met	Leu	Leu	Ala	Leu	Val	Cys	Leu	Leu	Ser	Cys	Leu	Leu	Pro	Ser
1				5					10					15

Ser	Glu	Ala	Lys	Leu	Tyr	Gly	Arg	Cys	Glu	Leu	Ala	Arg	Val	Leu
				20					25					30

His	Asp	Phe	Gly	Leu	Asp	Gly	Tyr	Arg	Gly	Tyr	Ser	Leu	Ala	Asp
				35					40					45

Trp	Val	Cys	Leu	Ala	Tyr	Phe	Thr	Ser	Gly	Phe	Asn	Ala	Ala	Ala
				50					55					60

Leu	Asp	Tyr	Glu	Ala	Asp	Gly	Ser	Thr	Asn	Asn	Gly	Ile	Phe	Gln
				65					70					75

Ile	Thr	Ser	Arg	Arg	Trp	Cys	Ser	Asn	Leu	Thr	Pro	Asn	Val	Pro
				80					85					90

Asn	Val	Cys	Arg	Met	Tyr	Cys	Ser	Asp	Leu	Leu	Asn	Pro	Asn	Leu
				95					100					105

Lys	Asp	Thr	Val	Ile	Cys	Ala	Met	Lys	Ile	Thr	Gln	Glu	Pro	Gln
				110					115					120

Gly	Leu	Gly	Tyr	Trp	Glu	Ala	Trp	Arg	His	His	Cys	Gln	Gly	Lys
				125					130					135

Asp	Leu	Thr	Glu	Trp	Val	Asp	Gly	Cys	Asp	Phe
				140					145	

<210> 222
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 222
gggatcatgt tgttggccct ggtc 24

<210> 223
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 223
gcaaggcaga cccagtcagc cag 23

<210> 224
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 224
ctgcctgcta cctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225
<211> 2049
<212> DNA
<213> Homo sapiens

<400> 225
agccgctgcc ccgggcgcgg cgccgcgcgc gccaccatga gtcccgcctc 50
gtgcttgagt tgcctgcgcc tctcctcttt cgcctctctt tcagccgcgc 100
cagcgaactg gctgacctg gccaaagtgt cgtcggcggg ggcgaactga 150
gaggaggaga cgtgcgagaa actcaagggc ctgatacaga ggcaggtgca 200
gatgtgcaag ccgaacctgg aagtcatgga ctccgtgcgc cgcggctgcc 250
agctggccat tgaggagtgc cagtcaccagt tccggaaccg gcgctggaac 300
tgctccacac tcgactcctt gcccgctctt gccaaagtggt tgacgcaagg 350
gactcgggag gcccctcttg tctacgcctt ctcttcggca ggtgtggcct 400
ttgcagtgaac gggggcgtgc agcagtgggg agctggagaa gtgcggctgt 450

gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500
ctctgacaac atcgccatcg gtgtggcctt ctcacagtcg tttgtggatg 550
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650
atgcaagtgc cacgggggtgt caggctcctg tgaggtaaag acgtgctggc 700
gagccgtgcc gcccttcgcg caggtgggtc acgcactgaa ggagaagttt 750
gatggtgcca ctgaggtgga gccacgccgc gtgggctcct ccagggcact 800
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ctggttttgt ttttgggtcc tcatgttatt tattgcgaa accaggcagg 1250
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300
ctgccactga ccaaagggac cttgctcgtg ccgctggctg ccgcctgtg 1350
gtgccactg accactcagt tggttatctg gtccgttttt ctacttcag 1400
acctaaagtg gagtaacaag gagtattacc accacatggc tactgacct 1450
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tcaaatgga ctctggcag cttgaacctc gaaqccatgt ctctcaaatg 1600
ccctgagaaa ggaacaagc agataccagg tcaagggcac caggttcatt 1650
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gcaagaagag ggagatgaga gcaagagac actgaagtc caccctagaa 1750
cccagcctgc ccagcctgc cctgggaag aaaaaactta accactccc 1800
agaccacct aggcagcat ataggctgc atcctggacc agggatccc 1850

gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950
acacacacac ggacacacac acacacctgc gagagagagg gaggaagg 2000
ctgtgccttt gcagtcatgc cccgagtcacc tttcacagca ctgttcctc 2049

<210> 226
<211> 351
<212> PRT
<213> Homo sapiens

<400> 226

Met	Ser	Pro	Arg	Ser	Cys	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Val	Phe	1	5	10	15
Ala	Val	Phe	Ser	Ala	Ala	Ala	Ser	Asn	Trp	Leu	Tyr	Leu	Ala	Lys	20	25	30	
Leu	Ser	Ser	Val	Gly	Ser	Ile	Ser	Glu	Glu	Glu	Thr	Cys	Glu	Lys	35	40	45	
Leu	Lys	Gly	Leu	Ile	Gln	Arg	Gln	Val	Gln	Met	Cys	Lys	Arg	Asn	50	55	60	
Leu	Glu	Val	Met	Asp	Ser	Val	Arg	Arg	Gly	Ala	Gln	Leu	Ala	Ile	65	70	75	
Glu	Glu	Cys	Gln	Tyr	Gln	Phe	Arg	Asn	Arg	Arg	Trp	Asn	Cys	Ser	80	85	90	
Thr	Leu	Asp	Ser	Leu	Pro	Val	Phe	Gly	Lys	Val	Val	Thr	Gln	Gly	95	100	105	
Thr	Arg	Glu	Ala	Ala	Phe	Val	Tyr	Ala	Ile	Ser	Ser	Ala	Gly	Val	110	115	120	
Ala	Phe	Ala	Val	Thr	Arg	Ala	Cys	Ser	Ser	Gly	Glu	Leu	Glu	Lys	125	130	135	
Cys	Gly	Cys	Asp	Arg	Thr	Val	His	Gly	Val	Ser	Pro	Gln	Gly	Phe	140	145	150	
Gln	Trp	Ser	Gly	Cys	Ser	Asp	Asn	Ile	Ala	Tyr	Gly	Val	Ala	Phe	155	160	165	
Ser	Gln	Ser	Phe	Val	Asp	Val	Arg	Glu	Arg	Ser	Lys	Gly	Ala	Ser	170	175	180	
Ser	Ser	Arg	Ala	Leu	Met	Asn	Leu	His	Asn	Asn	Glu	Ala	Gly	Arg	185	190	195	
Lys	Ala	Ile	Leu	Thr	His	Met	Arg	Val	Glu	Cys	Lys	Cys	His	Gly	200	205	210	
Val	Ser	Gly	Ser	Cys	Glu	Val	Lys	Thr	Cys	Trp	Arg	Ala	Val	Pro				

	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Thr Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
Glu Leu His Thr Cys Arg	350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 228

tggtggaga ctgtttaaat tatcggc 28

<210> 229

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 229

tgcttcgtca agtgccggca gtgccagcgg ctctgggagt t 41

<210> 230

<211> 1355

<212> DNA

<213> Homo sapiens

<400> 230

gggacgcgtg ggccggacgc tggggcgacg cgtgggcgga cgcgtgggct 50
gggtgcctgc atcgccatgg acaccaccag gtacagcaag tggggcgcca 100
gctccgagga ggtccccgga gggccctggg gacgctgggt gcactggagc 150
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200
ggctgtgatt ctgagtatcc tattgtccaa ggctccacg gagcgcgcgg 250
cgctgottga cggccacgac ctqctgagga caaacgcctc gaagcagacg 300
ggggcgctgg gtgccttgaa ggacnaatc cgaactgac acagctgctg 350
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400
cgcagggcaa gctgatggag caggagagcg cctgcggga actgcgtgag 450
cgcgtgaccc agggcttggc tgaagccggc aggggcccgt aggacgtccg 500
cactgagctg ttccgggcgc tggaggccgt gaggtccag aacaactcct 550
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tgccagcgcg cactgtgtga tegtggggg cctggatgag cagggttcc 700
tcaactcgaa cagcgtggc cgtgggttact ggctgggctt gagggctgtg 750
cgccatcttg gaaaggttca ggcctacag tgaatggaag gaatctctct 800
gggttcaa cctgggacg aggaagacg caatdaact tgggggngcg 850
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ccgcccagtg ccttggagcc gcgcccatg cagcatgtc tatcctgggg 1000
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tctcatca cagctgtg gtctcaaaa cacttgggc aacatagccc 1100
tgtccagccc agtgcctggg ctctgggacc tccatgcga cctcactcta 1150

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 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350
 aaaaa 1355

<210> 231

<211> 293

<212> PRT

<213> Homo sapiens

<400> 231

Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu
 1 5 10 15

Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg
 20 25 30

Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp
 35 40 45

Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg
 50 55 60

Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser
 65 70 75

Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp
 80 85 90

Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr
 95 100 105

Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu
 110 115 120

Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala
 125 130 135

Glu Ala Gly Arg Gly Arg Ala Asn Val Thr Thr Gln Leu Phe Arg
 140 145 150

Ala Leu Glu Ala Val Arg Leu Gln Asn Asn Ser Cys Glu Pro Cys
 155 160 165

Pro Thr Ser Trp Leu Ser Phe Glu Gly Ser Cys Tyr Phe Phe Ser
 170 175 180

Val Pro Lys Thr Thr Trp Ala Ala Ala Gln Asp His Cys Ala Asp
 185 190 195

Ala Ser Ala His Leu Val Ile Val Gly Gly Leu Asp Glu Gln Gly
 200 205 210

Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu
				215					220					225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val
				230					235					240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro
				245					250					255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr
				260					265					270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp
				275					280					285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys							
				290										

<210> 232

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 232

gcgagaactg tgtcatgatg ctgc 24

<210> 233

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 233

gtttctgaga ctcagcagcg gtgg 24

<210> 234

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

cacagtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gacaggggaa gagggtgata cgacccgggg aaagtcgctg ggcagggcga 50
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100
ctcccacgtc ctatctgoot ctogctggag gccaggccgt gcagcatcga 150
agacaggagg aactggagcc tcattggccg gcccggggcg ccggcctcgg 200
gcttaaatag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250
cgctcccgt gtcctgcgcg ggtgatggaa aaccccagcc cggccgcgc 300
cctgggcaag gccctctgcg ctctcctcct ggccaactct ggccgcgcgc 350
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400
tacagcatca ccttcacggg caagtggagc cagacggcct tccccagca 450
gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggcgc 500
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550
gggtgcgcg actttggga ggcgcgcac cctcgggcg tgatgaagga 600
gatcgaggcg gcgggggagg cgtgcagag cgtgcacgag gtgttttcgg 650
cgccgcgcgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700
cagcgcaggc actcgtcgt ctgctttgtg gtgcgcacg tgcccagccc 750
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ccgagggcac agggggtttc gcgtcctcc tgaccgcgtt gaggcgcgc 1400

cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450
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 gtctgtcttc agcctcctcc tctgcagga taaagtcac cccaaggctc 1550
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600
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 agcggggggc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys	1	5	10	15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly	20	25	30	
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile	35	40	45	
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr	50	55	60	
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala	65	70	75	
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val	80	85	90	
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala	95	100	105	
Leu	Met	Lys	Glu	Trp	Gln	Phe	Ala	Gly	Gln	Ala	Leu	Gln	Ser	Val	110	115	120	
His	Glu	Val	Phe	Ser	Ala	Pro	Ala	Val	Pro	Ser	Gly	Thr	Gly	Gln	125	130	135	
Thr	Ser	Ala	Glu	Leu	Glu	Val	Gln	Arg	Arg	His	Ser	Leu	Val	Ser	140	145	150	
Phe	Val	Val	Arg	Ile	Val	Pro	Ser	Pro	Asp	Trp	Phe	Val	Gly	Val	155	160	165	

Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala
170	175	180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala Gly Thr Asp Ser Gly Phe	
185	190	195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr Ile Pro Gln Asp Thr Val	
200	205	210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser His Pro Ala Asn Ser Phe	
215	220	225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro Pro Ile Ala Arg Val Thr	
230	235	240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg Ala Phe Ile Pro Pro Ala	
245	250	255
Pro Val Leu Pro	Ser Arg Asp Asn Glu Ile Val Asp Ser Ala Ser	
260	265	270
Val Pro Glu Thr	Pro Leu Asp Cys Glu Val Ser Leu Trp Ser Ser	
275	280	285
Trp Gly Leu Cys	Gly Gly His Cys Gly Arg Leu Gly Thr Lys Ser	
290	295	300
Arg Thr Arg Tyr	Val Arg Val Gln Pro Ala Asn Asn Gly Ser Pro	
305	310	315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu Cys Val Pro Asp Asn Cys	
320	325	330
Val		

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<214>

<215> Synthetic oligonucleotide probe

<400> 237

gaggaagcag agggagagag ag 22

<216> 238

<217> 18

<218> DNA

<219> Artificial Sequence

<220>

<221> Synthetic oligonucleotide probe

<400> 238

caggactcgc taagtcgc 18

<210> 239
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 239
cagccccccttc tctctcttttc tccc 24

<210> 240
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 240
gcagttatca gggacgcact cagcc 25

<210> 241
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 241
ccagcgagag gcagatag 18

<210> 242
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 242
cagccccccttc tctctcttttc tcccacgttc tctctgcttc tc 24

<210> 243
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 243
cagccccccttc tctctcttttc tcccacgttc tctctgcttc tc 42

<210> 244

<211> 1894
<212> DNA
<213> Homo sapiens

<400> 244

ggcggcgtcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50
tgtcttgctg gatattgaca aactgaagct ttctgcacc actggactta 100
aggaagagtg tactcgtagg cggacagctt tagtggcgg cgggccgctc 150
tcaccccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250
gctggagata ttgacataga gttgtggtcc aaagaagctc cttaaagcttg 300
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350
ttcatagagt tgtgcttggg ttcatagtc aaggcggaga tctactggc 400
acagggagtg gtggagagtc tatctatgga gcqccattca aagatgaatt 450
tcattcacgg ttggttttla atgggagagg atggtttacc atggcaaatg 500
ctggtttctca tgataatggc agccagtttt tcttcacact gggtcgagca 550
gatgaactta acaataagca taccatcttt ggaaaggtta caggggatac 600
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650
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tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaaacc 750
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aattttagtt 800
tactttcatt tggagaggaa gctgaggaag aagaggagga agtaaatcga 850
gttagtcaga gcattgaagg caaaagcaaa agtagtcatt acttgcttaa 900
ggatgatcca catctcagtt ctgttcnag ttgtaaaagt gaaaaaggtc 950
atgtaccaga ttatgttgtt tatctgagaa ataaaagttc aaadcatgat 1000
gaatatattg acggtggttc atgttcctt atgagaaaa aaatttccaa 1050
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 taacttttct tcacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<110> 245

<111> 472

<112> PRT

<113> Homo sapiens

<400> 245

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Leu	Leu	Lys	Thr	Thr	Ala	Gly	Asp	Ile	Asp	Ile	Glu	Leu	Trp	Ser
			20					25						30
Lys	Glu	Ala	Pro	Lys	Ala	Cys	Arg	Asn	Phe	Ile	Gln	Leu	Cys	Leu
			35					40						45
Glu	Ala	Tyr	Tyr	Asp	Asn	Thr	Ile	Phe	His	Arg	Val	Val	Pro	Gly
			50					55						60
Phe	Ile	Val	Gln	Gly	Gly	Asp	Pro	Thr	Gly	Ihr	Gly	Ser	Gly	Gly
			65					70						75
Glu	Ser	Ile	Tyr	Gly	Ala	Pro	Phe	Lys	Asp	Glu	Phe	His	Ser	Arg
			80					85						90
Leu	Arg	Phe	Asn	Arg	Arg	Gly	Leu	Val	Ala	Met	Ala	Asn	Ala	Gly
			95					100						105
Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala
			110					115						120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly
			125					130						135

Asp Thr Val Tyr Asn Met Leu Arg Leu Ser Glu Val Asp Ile Asp	140	145	150
Asp Asp Glu Arg Pro His Asn Pro His Lys Ile Lys Ser Cys Glu	155	160	165
Val Leu Phe Asn Pro Phe Asp Asp Ile Ile Pro Arg Glu Ile Lys	170	175	180
Arg Leu Lys Lys Glu Lys Pro Glu Glu Glu Val Lys Lys Leu Lys	185	190	195
Pro Lys Gly Thr Lys Asn Phe Ser Leu Leu Ser Phe Gly Glu Glu	200	205	210
Ala Glu Glu Glu Glu Glu Glu Val Asn Arg Val Ser Gln Ser Met	215	220	225
Lys Gly Lys Ser Lys Ser Ser His Asp Leu Leu Lys Asp Asp Pro	230	235	240
His Leu Ser Ser Val Pro Val Val Glu Ser Glu Lys Gly Asp Ala	245	250	255
Pro Asp Leu Val Asp Asp Gly Glu Asp Glu Ser Ala Glu His Asp	260	265	270
Glu Tyr Ile Asp Gly Asp Glu Lys Asn Leu Met Arg Glu Arg Ile	275	280	285
Ala Lys Lys Leu Lys Lys Asp Thr Ser Ala Asn Val Lys Ser Ala	290	295	300
Gly Glu Gly Glu Val Glu Lys Lys Ser Val Ser Arg Ser Glu Glu	305	310	315
Leu Arg Lys Glu Ala Arg Gln Leu Lys Arg Glu Leu Leu Ala Ala	320	325	330
Lys Gln Lys Lys Val Glu Asn Ala Ala Lys Gln Ala Glu Lys Arg	335	340	345
Ser Glu Glu Glu Glu Ala Pro Pro Asp Gly Ala Val Ala Glu Tyr	350	355	360
Arg Arg Val Tyr Gln Lys Thr Glu Ala Leu Arg Lys Gln Gln Ser	365	370	375
Lys Lys Gly Thr Ser Arg Glu Asp Gln Thr Leu Ala Leu Leu Asn	380	385	390
Gln Phe Lys Ser Lys Leu Thr Gln Ala Ile Ala Glu Thr Pro Glu	395	400	405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met	410	415	420

Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp
425 430 435

Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg
440 445 450

Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met
455 460 465

Arg Glu Lys Lys Glu Arg Arg
470

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

ggcgagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

caagttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

ggcgggagc aggaactgag 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249

caactgggaac aggaactgag atgtggatc 29

<210> 250

<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 250
ctgggttcagc agtgcaaggg tctg 24

<210> 251
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<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 251
cctctccgat taaaacgc 18

<210> 252
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 252
cagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253
<211> 2456
<212> DNA
<213> Homo sapiens

<400> 253
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tatttgccct tcttgacggc gtccacccct qcccagacat gtccacaggg 150
ttctccttgg ggtaggggac tctqgactcc acgacgtggc cggccgggca 200
gaccagcaca ggccgcgttt tctccttggg aacgggaaag tctagcaacc 250
ctctgtgggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300
actacatctg ctcttcaag tggttttgga accgggctct ttggatctaa 350
aactgccact gggttcactc taggaggaac aaatacaggt gccttgcaca 400
ccaagaggcc tcaagtggtc accaaatatg gaacctgca aggaataacag 450
atgcctgtgg ggaagacacc catccaactc ttcttaggag tccccttctc 500

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aaaaaa 2456

<210> 254
<211> 545
<212> PRT
<213> Homo sapiens

<400> 254
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Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly
35 40 45
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser
50 55 60
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly
65 70 75
Gln Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg
80 85 90
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met
95 100 105
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe
110 115 120
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro
125 130 135

Pro Glu Pro Trp	Lys Gly Ile Arg Asp	Ala Thr Thr Tyr Pro Pro	140	145	150
Gly Trp Ser Leu	Ala Leu Ser Pro Gly	Trp Ser Ala Val Ala Arg	155	160	165
Ser Arg Leu Thr	Ala Thr Ser Ala Ser	Arg Val Gln Ala Ser Leu	170	175	180
Leu Pro Gln Pro	Leu Ser Val Trp Gly	Tyr Arg Cys Leu Gln Glu	185	190	195
Ser Trp Gly Gln	Leu Ala Ser Met Tyr	Val Ser Thr Arg Glu Arg	200	205	210
Tyr Lys Trp Leu	Arg Phe Ser Glu Asp	Cys Leu Tyr Leu Asn Val	215	220	225
Tyr Ala Pro Ala	Arg Ala Pro Gly Asp	Pro Gln Leu Pro Val Met	230	235	240
Val Trp Phe Pro	Gly Gly Ala Phe Ile	Val Gly Ala Ala Ser Ser	245	250	255
Tyr Glu Gly Ser	Asp Leu Ala Ala Arg	Glu Lys Val Val Leu Val	260	265	270
Phe Leu Gln His	Arg Leu Gly Ile Phe	Gly Phe Leu Ser Thr Asp	275	280	285
Asp Ser His Ala	Arg Gly Asn Trp Gly	Leu Leu Asp Gln Met Ala	290	295	300
Ala Leu Arg Trp	Val Gln Glu Asn Ile	Ala Ala Phe Gly Gly Asp	305	310	315
Pro Gly Asn Val	Thr Leu Phe Gly Gln	Ser Ala Gly Ala Met Ser	320	325	330
Ile Ser Gly Leu	Met Met Ser Pro Leu	Ala Ser Gly Leu Phe His	335	340	345
Arg Ala Ile Ser	Gln Ser Gly Thr Ala	Leu Phe Arg Leu Thr Ile	350	355	360
Thr Ser Asp Pro	Leu Lys Val Ala Lys	Lys Val Ala His Leu Ala	365	370	375
Gly Cys Asn His	Asn Ser Thr Gln Ile	Leu Val Asn Cys Leu Arg	380	385	390
Ala Leu Ser Gly	Thr Lys Val Met Arg	Val Ser Asn Lys Met Arg	395	400	405
Phe Leu Gln Leu	Asn Phe Gln Arg Asp	Pro Glu Glu Ile Ile Trp	410	415	420

Ser Met Ser Pro Val Val Asp Gly Val Val Ile Pro Asp Asp Pro	425	430	435
Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu	440	445	450
Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn	455	460	465
Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp	470	475	480
Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met	485	490	495
Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr	500	505	510
Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala	515	520	525
Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu	530	535	540
Pro Gln Glu Trp Ala	545		

<210> 255
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 255
 aggtgactgc aggagtcttg ggg 23

<210> 256
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 256
 ccacccagg aagcgaaga tgc 24

<210> 257
 <211> 45
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 257

gaacggtana agtggctccg cttcagcgag gactgtctgt acctg 45

<210> 258

<211> 2764

<212> DNA

<213> Homo sapiens

<400> 258

gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50

actgcactg ctgtgtcct cgtgtctggg cgggtcccag gctatggatg 100

ggagattctg gatacgagtg caggagtcag tgatggtgcc ggagggcctg 150

tgcattcttg tgcctgtct tttctctac ccccgacaag actggacagg 200

gtctacccca gcttatggct actgggtcaa agcagtgact gagacaacca 250

aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300

accgggggccc gattccagct cactggggat cccggcaagg ggaactgtct 350

cttgggtgatc agadaacccc aactccaggc tgaatcacag taattctttc 400

gggtggagag aggaagctat gtgacatata atttcattgaa cgatgggttc 450

tttctaaaag taacagtgtc cagcttcacg cccagacccc aggaccacaa 500

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agaggaccgt ccgactccgt gtggcctatg ccccagaga ccttggtatc 600

agcatttcac gtgacaacac gccagccctg gagccccaga cccagggaaa 650

tgtcccatac ctggaagccc aaaaaggcca gttcctgccc ctctctgtg 700

ctgtgacag ccagccccc cccacactga gctgggtcct gcagaacaga 750

gtcctctcct cgtcccatac ctggggccct agaccctgg ggttgagct 800

gcccggggtg aaggctggg atttagggg ctatccctac ccaggggaga 850

ccagcttag ctccacacag ccaggggtga actctctat ccagtatct 900

ctg gcttc tgcactgct cgtttccaa gcaaacada caatcctgga 950

aaactttggg aaggccact ctctccact actggaaggc caaagcctgt 1000

gcttgtctg tgtcacacac agcagggccc cagccaggtt gacctgacc 1050

cagaggggac aggtttctg cccctcccag cctcagacc cgggggtcct 1100

ggagctgctt cgggttcaa tggagacaa agcagagttc acctgcaacg 1150

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tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250
aatcggcacc acggctcttc ttttctctg cctggccctg atcatcatga 1300
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cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600
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tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggaggt 2050
tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100
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aaaacagatt gcagtaaaga agccaacca atcccacca aaccaagttg 2500
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agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700

ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

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Ala	Met	Asp	Gly	Arg	Phe	Trp	Ile	Arg	Val	Gln	Glu	Ser	Val	Met	
				20					25					30	
Val	Pro	Glu	Gly	Leu	Cys	Ile	Ser	Val	Pro	Cys	Ser	Phe	Ser	Tyr	
				35					40					45	
Pro	Arg	Gln	Asp	Trp	Thr	Gly	Ser	Thr	Pro	Ala	Tyr	Gly	Tyr	Trp	
				50					55					60	
Phe	Lys	Ala	Val	Thr	Glu	Thr	Thr	Lys	Gly	Ala	Pro	Val	Ala	Thr	
				65					70					75	
Asn	His	Gln	Ser	Arg	Glu	Val	Glu	Met	Ser	Thr	Arg	Gly	Arg	Phe	
				80					85					90	
Gln	Leu	Thr	Gly	Asp	Pro	Ala	Lys	Gly	Asn	Cys	Ser	Leu	Val	Ile	
				95					100					105	
Arg	Asp	Ala	Gln	Met	Gln	Asp	Glu	Ser	Gln	Tyr	Phe	Phe	Arg	Val	
				110					115					120	
Glu	Arg	Gly	Ser	Tyr	Val	Thr	Tyr	Asn	Phe	Met	Asn	Asp	Gly	Phe	
				125					130					135	
Phe	Leu	Lys	Val	Thr	Val	Leu	Ser	Phe	Thr	Pro	Arg	Pro	Gln	Asp	
				140					145					150	
His	Arg	Thr	Asp	Leu	Thr	Cys	His	Val	Asp	Phe	Ser	Arg	Lys	Gly	
				155					160					165	
Val	Ser	Ala	Gln	Arg	Thr	Val	Arg	Leu	Arg	Val	Ala	Tyr	Ala	Pro	
				170					175					180	
Arg	Asp	Leu	Val	Ile	Ser	Ile	Ser	Arg	Asp	Asn	Thr	Pro	Ala	Leu	
				185					190					195	
Glu	Pro	Gln	Pro	Gln	Gly	Asn	Val	Pro	Tyr	Leu	Glu	Ala	Gln	Lys	
				200					205					210	
Gly	Gln	Phe	Leu	Arg	Leu	Leu	Cys	Ala	Ala	Asp	Ser	Gln	Pro	Pro	
				215					220					225	

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser	230	235	240
His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val	245	250	255
Lys Ala Gly Asp Ser Gly Arg Tyr Thr Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln Gln Arg Ala Leu Asp Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu Arg Val Met Val Ser Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu Gly Asn Gly Thr Ser Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys Leu Val Cys Val Thr His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp Thr Gln Arg Gly Gln Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro Gly Val Leu Glu Leu Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu Phe Thr Cys His Ala Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser Leu Ser Leu Ser Val His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala Phe Ser Asn Gly Ala Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu Phe Leu Cys Leu Ala Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg Arg Thr Gln Thr Glu Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser Thr Ile Leu Asp Tyr Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu Ala Gln Lys Arg Asn Gln Lys Ala Thr Ile Asn	455	460	465
Ser Pro Arg Thr Pro Pro Pro Pro Gly Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln Lys Lys Gln Tyr Gln Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser Thr Gln Ala Pro Glu Ser Gln Glu Ser Gln Glu	500	505	510

Glu Leu His Tyr Ala Thr Leu Asn Phe Pro Gly Val Arg Pro Arg
 515 520 525

Pro Glu Ala Arg Met Pro Lys Gly Thr Gln Ala Asp Tyr Ala Glu
 530 535 540

Val Lys Phe Gln

<210> 260

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 260

caaagcctgc gcctggctctg tg 22

<210> 261

<211> 24

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 261

ttctggagcc cagagggtgc tgag 24

<210> 262

<211> 45

<212> RNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 262

uaatttccca cccattcaaa tggagcacca aggagagttc acctg 45

<210> 263

<211> 357

<212> RNA

<213> Homo sapiens

<400> 263

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actgtctgctg tttatgttgg gaattcctct cctatggcct tgtcttggag 100

caacagaaaa ctctcaaaac aagaaagtc aagagacagt gggatctcat 150

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<210> 264

<211> 772

<212> PRT

<213> Homo sapiens

<400> 264

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Leu	Trp	Pro	Cys	Leu	Gly	Ala	Thr	Glu	Asn	Ser	Gln	Thr	Lys	Lys		20	25	30	
Val	Lys	Gln	Pro	Val	Arg	Ser	His	Leu	Arg	Val	Lys	Arg	Gly	Trp		35	40	45	
Val	Trp	Asn	Gln	Phe	Phe	Val	Pro	Glu	Glu	Met	Asn	Thr	Thr	Ser		50	55	60	
His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75	
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90	
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105	
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120	
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135	
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150	
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165	
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180	
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195	
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210	
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225	
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240	
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255	
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270	
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285	

Gly Glu Asn Ala Glu Met Asp Tyr Ser Ile Glu Glu Asp Asp Ser	290	295	300
Gln Thr Phe Asp Ile Ile Thr Asn His Glu Thr Gln Glu Gly Ile	305	310	315
Val Ile Leu Lys Lys Lys Val Asp Phe Glu His Gln Asn His Tyr	320	325	330
Gly Ile Arg Ala Lys Val Lys Asn His His Val Pro Glu Gln Leu	335	340	345
Met Lys Tyr His Thr Glu Ala Ser Thr Thr Phe Ile Lys Ile Gln	350	355	360
Val Glu Asp Val Asp Glu Pro Pro Leu Phe Leu Leu Pro Tyr Tyr	365	370	375
Val Phe Glu Val Phe Glu Glu Thr Pro Gln Gly Ser Phe Val Gly	380	385	390
Val Val Ser Ala Thr Asp Pro Asp Asn Arg Lys Ser Pro Ile Arg	395	400	405
Tyr Ser Ile Thr Arg Ser Lys Val Phe Asn Ile Asn Asp Asn Gly	410	415	420
Thr Ile Thr Thr Ser Asn Ser Leu Asp Arg Glu Ile Ser Ala Trp	425	430	435
Tyr Asn Leu Ser Ile Thr Ala Thr Glu Lys Tyr Asn Ile Glu Gln	440	445	450
Ile Ser Ser Ile Pro Leu Tyr Val Gln Val Leu Asn Ile Asn Asp	455	460	465
His Ala Pro Glu Phe Ser Gln Tyr Tyr Glu Thr Tyr Val Cys Glu	470	475	480
Asn Ala Gly Ser Gly Gln Val Ile Gln Thr Ile Ser Ala Val Asp	485	490	495
Arg Asp Glu Ser Ile Glu Glu His His Phe Tyr Phe Asn Leu Ser	500	505	510
Val Glu Asp Thr Asn Asn Ser Ser Phe Thr Ile Ile Asp Asn Gln	515	520	525
Asp Asn Thr Ala Val Ile Leu Thr Asn Arg Thr Gly Phe Asn Leu	530	535	540
Gln Glu Glu Pro Val Phe Tyr Ile Ser Ile Leu Ile Ala Asp Asn	545	550	555
Gly Ile Pro Ser Leu Thr Ser Thr Asn Thr Leu Thr Ile His Val	560	565	570

Cys	Asp	Cys	Gly	Asp	Ser	Gly	Ser	Thr	Gln	Thr	Cys	Gln	Tyr	Gln	575	580	585
Glu	Leu	Val	Leu	Ser	Met	Gly	Phe	Lys	Thr	Glu	Val	Ile	Ile	Ala	590	595	600
Ile	Leu	Ile	Cys	Ile	Met	Ile	Ile	Phe	Gly	Phe	Ile	Phe	Leu	Thr	605	610	615
Leu	Gly	Leu	Lys	Gln	Arg	Arg	Lys	Gln	Ile	Leu	Phe	Pro	Glu	Lys	620	625	630
Ser	Glu	Asp	Phe	Arg	Glu	Asn	Ile	Phe	Gln	Tyr	Asp	Asp	Glu	Gly	635	640	645
Gly	Gly	Glu	Glu	Asp	Thr	Glu	Ala	Phe	Asp	Ile	Ala	Glu	Leu	Arg	650	655	660
Ser	Ser	Thr	Ile	Met	Arg	Glu	Arg	Lys	Thr	Arg	Lys	Thr	Thr	Ser	665	670	675
Ala	Glu	Ile	Arg	Ser	Leu	Tyr	Arg	Gln	Ser	Leu	Gln	Val	Gly	Pro	680	685	690
Asp	Ser	Ala	Ile	Phe	Arg	Lys	Phe	Ile	Leu	Glu	Lys	Leu	Glu	Glu	695	700	705
Ala	Asn	Thr	Asp	Pro	Cys	Ala	Pro	Pro	Phe	Asp	Ser	Leu	Gln	Thr	710	715	720
Tyr	Ala	Phe	Glu	Gly	Thr	Gly	Ser	Leu	Ala	Gly	Ser	Leu	Ser	Ser	725	730	735
Leu	Glu	Ser	Ala	Val	Ser	Asp	Gln	Asp	Glu	Ser	Tyr	Asp	Tyr	Leu	740	745	750
Asn	Glu	Leu	Gly	Pro	Arg	Phe	Lys	Arg	Leu	Ala	Cys	Met	Phe	Gly	755	760	765
Ser	Ala	Val	Gln	Ser	Asn	Asn									770		

<210> 265

<211> 349

<212> RNA

<213> Homo sapiens

<220>

<221> unsure

<222> 24, 60, 141, 226, 228, 249, 252

<223> unknown base

<400> 265

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gaatattttt taaaatggat agagaactgc aagatgagta ttgggtaac 100

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aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200
aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250
tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300
aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg cacc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

caactacgtt attacaccaa aagttaaaaa caatcatggt tcttgaggaa 50

aa 10

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

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caaaacgagc aagaaagctc tctcagagaa caaaacgagc aacagggctc 100

caagccttaa cttcctccgc ggggcaccgc caccttcggg agtcggggtt 150

gcccacctgc aaactctccg ccttctgcac ctgccacccc tgagccagcg 200
cgggcccccg agcgagtcac ggccaacgcg gggctgcagc tgttgggctt 250
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gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400
gatccagtgc aaagtctttg actccttgcg gaatctgagc agcacattgc 450
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<210> 270

<211> 211

<212> PRT

<213> Homo sapiens

<400> 270

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Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp

20										25					30				
Arg	Ile	Tyr	Ser	Tyr	Ala	Gly	Asp	Asn	Ile	Val	Thr	Ala	Gln	Ala					
				35					40					45					
Met	Tyr	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Ser	Gln	Ser	Thr	Gly					
				50					55					60					
Gln	Ile	Gln	Cys	Lys	Val	Phe	Asp	Ser	Leu	Leu	Asn	Leu	Ser	Ser					
				65					70					75					
Thr	Leu	Gln	Ala	Thr	Arg	Ala	Leu	Met	Val	Val	Gly	Ile	Leu	Leu					
				80					85					90					
Gly	Val	Ile	Ala	Ile	Phe	Val	Ala	Thr	Val	Gly	Met	Lys	Cys	Met					
				95					100					105					
Lys	Cys	Leu	Glu	Asp	Asp	Glu	Val	Gln	Lys	Met	Arg	Met	Ala	Val					
				110					115					120					
Ile	Gly	Gly	Ala	Ile	Phe	Leu	Leu	Ala	Gly	Leu	Ala	Ile	Leu	Val					
				125					130					135					
Ala	Thr	Ala	Trp	Tyr	Gly	Asn	Arg	Ile	Val	Gln	Glu	Phe	Tyr	Asp					
				140					145					150					
Pro	Met	Thr	Pro	Val	Asn	Ala	Arg	Tyr	Glu	Phe	Gly	Gln	Ala	Leu					
				155					160					165					
Phe	Thr	Gly	Trp	Ala	Ala	Ala	Ser	Leu	Cys	Leu	Leu	Gly	Gly	Ala					
				170					175					180					
Leu	Leu	Cys	Cys	Ser	Cys	Pro	Arg	Lys	Thr	Thr	Ser	Tyr	Pro	Thr					
				185					190					195					
Pro	Arg	Pro	Tyr	Pro	Lys	Pro	Ala	Pro	Ser	Ser	Gly	Lys	Asp	Tyr					
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Val

<10> 271

<11> 564

<12> DNA

<13> homo sapiens

<20>

<21> unsure

<22> 21, 69, 163, 434, 436, 444

<23> unknown base

<400> 271

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ctccctatgc tggcgcacaac atcgtgaccg cccagcccat gtacgagggg 150

ctgtggatgt ccngcgtgtc gcagagcacc gggcagatcc agtgcaaagt 200
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250
 tgatggtggt tggcaccctc ctgggagtga tagcaatctt tgtggccacc 300
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400
 ttttagttgc cacagcatgg tatggcaata gaancttca acantctat 450
 gacctatga cccagtcaa tgccaggtae gaatttggtc aggctctctt 500
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550
 gctgttctg tccc 564

<210> 272

<211> 498

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341

<223> unknown base

<400> 272

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 cntcagcaact gccctgcgcc agtggaggat ttactcttat nccggnaca 150
 acatcgtgac cgcgcaggcc ntgtacgagg ggctgtggat gtctgcgtg 200
 tgcagagca ccgggcagat ccagtgcaaa gtctttgact cccttgetga 250
 atctgagcag cacattgcaa gcaaccctg ccttgatggt ggttggcatc 300
 ctctgggag tgatagcaat cttnntggcc accgttgtnn ntgaagtga 350
 gaag gctt ggaagagat gaggtggaga aatcagat ggtgt att 400
 agggggcgga tattctctct tgcaggtctg gttactctag tgcacacaga 450
 atggtatggc aatagaatcg ttcaagaatt ctatgacct atgacaga 498

<210> 273

<211> 552

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394
<223> unknown base

<400> 273

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gatgaanccg gccatentca gactccctgc cccatggaga tttnnccat 100
gctggcgaca acatentgac cccagccat gtacgagggg ctttgaacgt 150
engcgtgtcg cagancaccg ggcagatcca gtgcaaagtc tttgactcct 200
tgetgaatct gngcagcaca ttgcagcaac ccttgccctg atggtggttg 250
gcctcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300
tgtatgaagt gottggaaga cgatgaggtg cagaagatga ggatggctgt 350
cattggggggc gcgatatttc ttcttgccagg tctggctatt tnnngttgcc 400
acagcatggt atggcaatag aatcggtcaa gaattctatg accctatgac 450
cccagtcatt gccaggtacg aatttggtca ggcctctctc actggctggg 500
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ga 552

<210> 274

<211> 526

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407

<223> unknown base

<400> 274

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ccattgcaaa ctctttgaat ccttgcctgaa tctgagcagc acattgcaag 200
caaccctgac cttgatgggg ttggcctcct cctgggagtg atagcaacct 250
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gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350
caggtctgga ctttttagtn ggcacagcat cctatggcaa tagantnntt 400
cnnnnntct atgacctat gaccccagtc aatgcacaggt acgaatttgg 450

tcaggctctc ttcactggct gggtgctgc ttctctctgc cttctgggag 500

gtgccctact ttgctgttcc tgtccc 526

<210> 275

<211> 398

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274

<223> unknown base

<400> 275

agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50

gcagcacatt ncaagcaacc ccttgcccttg aaggtgggtg ncatccccc 100

tgggagtga tagcaatctt tgtggccacc gttggcatga agtntatgaa 150

gtgcttggaa gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

atgcatatt tcttcttaca ggtctageta ttttagttnn cacagcatgg 250

tatggcaata gnatnnttcg nggnttctat gacctatga cccagtcaa 300

tggcaggtae gaatttggtc aggtctctct cactggctgg gctgctgctt 350

ctctctgctt tctgggaggt gccctacttt gctgttcttg tccccgaa 398

<410> 276

<411> 495

<412> DNA

<413> Homo sapiens

<420>

<421> unsure

<422> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476

<423> unknown base

<430> 276

atcaatgccc tgcctccagt ggaggattaa ttcttatgnt ggggacaaca 50

ttgtgaatgc ccaggccatg taaggggggc tctggatgta cggggtgttg 100

cagagcaccg ggcagatcca gtgcataagtn ttgactctt tgetgaattt 150

gagcagcaca ttgcaagcaa cccgtgcctt gatgggtggtt ggcattcttc 200

tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250

tgtttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300

cgggatattt cttnltgcag gtctggtctat tttagtgtcc acagcatggt 350

atggcaatag aatnqticaa gaattttatg acctatgac cccagtcaat 400

gccaggtacg aatttgggtca ggctttnttc actggctggg ctgctgcttn 450

tttctgcctt ntgggaggtg ccctantttg ctgttctctg gaacc 495

<210> 277

<211> 200

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 34, 87, 138, 147, 163, 165-166, 172

<223> unknown base

<400> 277

tcataggggg ggcgatatt ttttcttgca ggtntggta ttttagttgc 50

cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100

ccccagtcaa tgccaggtac gaatttggtc aggctctntt cactggntgg 150

gtgctgctt ctntnngcct tntgggaggt gccctacttt gctgttctg 200

<210> 278

<211> 542

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396

<223> unknown base

<400> 278

ttcttgggat ggatccgcc ccattentac atgcectgcc ccttgagat 50

ttactctat gctggcgaac aacatentga ccgccaggc catgtacgag 100

gggctgtgga atgtctgcg tgtcccagag caccgggcag atccagtga 150

aagtcttga ctcttgcgt aatctdaga ccacattga agcaacnta 200

ctttatagt aattacata ctcttggag taatadcaat ctttgtggc 250

acatttaca taaaagtata taaatcctt aaaaacacat aaggtacaa 300

agatgaggat ggctgtcatt gggggcgcga tatttctct tgcaggctctg 350

gctattttag nngccacagc atgggtatggc aatcagaccc nntcanaaac 400

tctatgaccc tatgacccca gtcaatgcca ggtaogaatt tggtcaggct 450

ctcttcaactg gctgggctgc tgccttctct tgccttctgg gaggtgacct 500

aatttgctgt tctgtcccc gaaaaacaac ctcttaccba cg 542

<210> 279
<211> 548
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 90, 115, 147, 228, 387
<223> unknown base

<400> 279
ggggggtgca gctgttgggc ttcattctgc ttcttgggat ggaatcggcg 50
ccatggtcag cactgccctg ccccatggag gatttactcn tatgctggcg 100
acaacatcgt gaccncccag gccatgtacg aggggctgtg gatgtcngcg 150
tgctgcagag caccgggcag atccagtga aagtctttga ctcttctgtg 200
aatctgagca gcacattgca agcaacctg ccttgatggg ggttggcctc 250
ctcttgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300
gaagtgttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350
gggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400
atggtatggc aatagaatcg ttcaagaatt ctatgacct atgaccccag 450
tcaatgccag gtacgaattt ggtcaggctc tcttcaactg ctgggctgct 500
gcttctctct gccttctggg aggtgcacct ctttctgtgt cctgcgaa 548

<210> 280
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 280
caagcagtc atggccaacg c 21

<210> 281
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 281
gttgcacag tagttttca cgttgg 26

<210> 282
<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 282

ctgcagctgt tgggcttcat tctgccttc ctgggatgga tcg 43

<210> 283

<211> 2285

<212> DNA

<213> Homo sapiens

<400> 283

gcgtgccgtc agctgcgcg gcacgcggc ctgcacctcg cctccgccc 50
ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccaccccg 100
tagaggaccc ccgcccgtgc ccgacccggt ccccgcttt ttgtaaaact 150
taaagcgggc gcagcattaa cgcttccgc ccgggtgacc tctcaggggt 200
ctcccgcca aaggcgctcc gcgcctaagg aacatggcga aggtggagca 250
ggtcctgagc ctgcagccgc agcacgagct caaatccga ggctccctca 300
ccgatgttgt caccaccaac ctaaagcttg gcaaccgcac agaccgaaat 350
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400
caacagcggg atcatcgatg caggggcctc aattaatgta tctgtgatgt 450
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500
gttcagtcta tgtttgcctc aactgacact tcagatatgg aagcagtatg 550
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600
ttgaattgcc agcagagaat gataaacac atgatgtaga aataaataaa 650
attatatcca caactgcac aaagacaaa acaccaatag tgtctaatgc 700
tctgagttct tctttggatg acacgaag* taagaagggt atggaagaat 750
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800
ttcaaggaag aagatggact gcgcatgagg aagacagtgc agagcaacag 850
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900
ggctcttggc tctggtggtt ttgttctta tcttgggtgt aattattggg 950
aagattgctt tgtagaggta gcatgcacag gatggtaa at tggattgggtg 1000
gatccaccat atcatgggat tttaatttat cataaccatg tgtaaaaaga 1050

aattaatgta tgatgacatc tcacaggtct tgcctttaaa ttacccctcc 1100
atgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150
ttagaaagtt aaaaatgtat agtaactgat tgaggggggaa aaagaatgat 1200
ctttattaat gacaagggaa accatgagta atgccacaat ggcataattgt 1250
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300
tctcttaaaa tgacaccctt cctcgccctg tgggtgctggc ccttggggag 1350
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acgtggccca ctcccgccc aggtgcttt cctgtctctt agttctgtcc 1450
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ttgcactgtg gcagcatcag acgtactcgt cataagttag aggcgtgtgt 1550
tgactgattg acccagcgtt ttggaaataa atggcagtgc tttgttact 1600
taaagggacc aagctaaatt tgtattggtt catgtagtga agtcaaactg 1650
tattccagag atgtttaatg catatttaa ttatttaag ttttccct 1700
catgttttct tattgtcaca agagtacagt taatgctgctg tctgctgaa 1750
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ctctggagag tctggtcatg tggaggtggg gtttattggg atgctggaga 1850
agaactgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050
agacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100
ggaggggaa cagcagttgt ggggggggag cagggggaaga gagaaactct 2150
tgcctcctat ctttataat tcttcaaa ttggaaggc tcttctct 2200
tgcctcctat tcttataat tcttcaaa ttggaaggc tcttctct 2250
-gaaaaatta taataaagcc ccaaatttaa gaaaa 2291

<110> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met Ala Lys Val Glu Gln Val Leu Ser Leu Glu Pro Gln His Glu

1	5	10	15
Leu Lys Phe Arg Gly Pro Phe Thr Asp Val Val Thr Thr Asn Leu	20	25	30
Lys Leu Gly Asn Pro Thr Asp Arg Asn Val Cys Phe Lys Val Lys	35	40	45
Thr Thr Ala Pro Arg Arg Tyr Cys Val Arg Pro Asn Ser Gly Ile	50	55	60
Ile Asp Ala Gly Ala Ser Ile Asn Val Ser Val Met Leu Gln Pro	65	70	75
Phe Asp Tyr Asp Pro Asn Glu Lys Ser Lys His Lys Phe Met Val	80	85	90
Gln Ser Met Phe Ala Pro Thr Asp Thr Ser Asp Met Glu Ala Val	95	100	105
Trp Lys Glu Ala Lys Pro Glu Asp Leu Met Asp Ser Lys Leu Arg	110	115	120
Cys Val Phe Glu Leu Pro Ala Gln Asn Asp Lys Pro His Asp Val	125	130	135
Glu Ile Asn Lys Ile Ile Ser Thr Thr Ala Ser Lys Thr Glu Thr	140	145	150
Pro Ile Val Ser Lys Ser Leu Ser Ser Ser Leu Asp Asp Thr Glu	155	160	165
Val Lys Lys Val Met Glu Glu Cys Lys Arg Leu Gln Gly Glu Val	170	175	180
Gln Arg Leu Arg Glu Glu Asn Lys Gln Phe Lys Glu Glu Asp Gly	185	190	195
Leu Arg Met Arg Lys Thr Val Gln Ser Asn Ser Pro Ile Ser Ala	200	205	210
Leu Ala Pro Thr Gly Lys Glu Glu Gly Leu Ser Thr Arg Leu Leu	215	220	225
Ala Leu Val Val Leu Phe Phe Ile Val Gly Val Ile Thr Thr Lys	230	235	240

Ile Ala Leu

<210> 285

<211> 418

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 40, 53, 68, 119, 134, 177-178, 255

<223> unknown base

<400> 285

gtcagttcttc tagattgtcc ttatcccacc ttccaaccan tactcacatt 50
tenagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100
ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150
cagcagttttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200
cttctagtag tagttgagag ttgactgtg aattaatttt atgccataaa 250
agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300
taataaagcc ccaaaattaa gaattctttt gtcattttgt cacatttgct 350
ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400
gttaacttta aaatgagc 418

<210> 286

<211> 543

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 73, 97

<223> unknown base

<400> 286

tattgtaaaag gccattttaa accattggta ggccctggta catgatgctg 50
gattacctcc ttaaatgaca ccttcctcg cctgttggtg ctggccnttg 100
gggagctgga gcccagcat gctggggagt gcggtcagct ccacacagta 150
gtcccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250
aaggaaftgc cactctgga gccatcagac tactcgtcat aatgagagg 300
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgttt 350
gttcaactta aqqaccaa qctaaattgta ttggttcacg tagtgaagtc 400
aaactgttat tcagagatgt ttaatgcata ttttaacttat ttaatgtatt 450
tcactctcat tttcttatt gtcacaagag tacagttaat gctgcgtgct 500
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242
<223> unknown base

<400> 287
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ctttagagagg tagnatgcac cnggctggta aattggattg gtggatccac 100
catatccatg ggatttaaatt ttatcataac catgtgtaaa aagaaattaa 150
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250
agttaaaaaat gtatagtaac 270

<210> 288
<211> 428
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 35, 116, 129, 197, 278, 294, 297, 349, 351
<223> unknown base

<400> 288
ggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50
gcaatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100
gcaactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150
actgattgac ccagcgcttt ggaaataaat gccagtgtt tgttcantta 200
aagggaacca gctaaatttg tattggttca tgtagtgaag tcaaactgtt 250
attcagagat gttaaagca tatttaantt atttaatgta tttnatntca 300
tgtctcttta ttgtcacaag agtacagtta atgctggctg ctgctgaant 350
ctcctgggag ccttgggact gttgttggtg gttgtgaa tttttatctt 400
cttgatgctc tggatcgtg gacataga 428

<210> 289
<211> 320
<212> DNA
<213> Homo sapiens

<400> 289
tgctttccgt gcttccagtt ctgtccaaag catcagctcc ttgggaactg 50

atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagaag 100
 tactgtcat aagtgaagg cgtgtgttga ctgattgacc cagcggtttg 150
 gaaataaatg gcagtgcctt gtccacttaa agggaccaag cttaaattgt 200
 attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250
 atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300
 gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,
 447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacatttaa aagttgaggg gaaaagattg atccttttatt aatgacaagg 50
 gaaaacntgn gtaatgcac aatggcatat tgtaaattgc attttaaaca 100
 ttggtaggcc ttggtacatg atgctggatt acctctctta aaatgacacc 150
 ctccctcgcc tgttggtgct ggcccttggg gagctngagc ccagcatgct 200
 ggggagtgcg gtctgtcca cacagtagtc ccangtggc ccantcccg 250
 ccaggtgc tttcgtgtc ttcagttctg tccaagccat cagctccttg 300
 ggantgatga acagagtcag aagcccaag gaattgcant gtggcagcat 350
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccagc 400
 gctttgaaa taaatggcag tctttgttc anttaaaggg nccaagntaa 450
 atttgattg gtccatgtag tgaagtcaaa atgtatttca gagatgttta 500
 atgatatat aattattca acatattca tttatgttc acctatgttc 550
 atgggtg atgtatggt ggtgtgtgt gaatttgc tggggaattg 600
 gtattgctg 609

<210> 291

<211> 493

<212> DNA

<213> Homo sapiens

<400> 291

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 cacagtagtc cccacgtggc ccactcccgg cccaggetgc tttccgtgtc 100
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200
 gagaggcgtg tgttgactga ttgaccagc gctttggaaa taaatggcag 250
 tgctttgttc acttaaaggg accaagctaa atttgtattg gtcatgtag 300
 tgaagtcaaa ctgttattca gagatgttta atgcataatt aacttattta 350
 atgtatttca tctcatgttt tcttattgtc acaagagtac agttaatgct 400
 gcgtgctgct gaactctgtt ggggtgaactg gtattgctgc tggagggctg 450
 tgggctcctc tgtctctgga gagtctggtc atgtggaggt ggg 493

<210> 292

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 292

gcaccaccgt aggtacttgt gtgagga 27

<210> 293

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aacaccaga gccagagcc ggg 23

<210> 294

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcggaatc atcgatgcag gggccccaat caatgatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

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ggctggctga gaggtccca gctgcagcgt ccccgccgc ctctcgga 100
gctctgatct cagctgacag tgccctcggg gaccaaaca gcctggcagg 150
gtctcacttt gttgcccagg ctggagttca gtgccatgat catggtttac 200
tgcagccttg acctcctggg ttcaagcgat cctgctgagt agctgggact 250
acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300
atttttcacc cctgggtgga cctcattga tggatctgaa atggaatggg 350
attttatgtg gcacttgaga aaggtagccc ggattgtcag tgaaaggact 400
ttccatctca ccagcccgcc atttgaggca gatgctaaga tgatggtaaa 450
tacagtgtgt ggcctcgaat gccagaaaaga actcccaact cccagccttt 500
ctgaattgga ggattatctt tccatgaga ctgtctttga gaatggcacc 550
cgaaacttaa ccagggtgaa agttcaagat ttggtcttg agccgaactca 600
aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgatg 650
gcaccgacag caggttcagc atcttgga aaaggttctt aaccaatttc 700
cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750
tccccctcag catgtttctaa ctgctgccc ctgtgttcat gatggaaagg 800
actatgtcaa agggagtaaa aagctaaggg tagggttgtt gaagatgagg 850
aataaaagtg gaggaagaa acgtcgaggt tctaagagga gcaggagaga 900
agctagtggg ggtgaccaa gagagggtac cagagagcat ctgcaggaga 950
gaggaagggt tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000
gcgaaggga ggcttctt tcagtggac cgggtcaaga atacccacat 1050
tcgaagggt tgggacgag gaggaatgg aaaggtacc ttggaactatg 1100
actatgctct tctggagctg aagcgtgctc aaaaaagaa atacatggaa 1150
cttggaatca gcccacgat caagaaaatg cctgggtggaa tgatccactt 1200
ctcaggattt gataacgata gggctgatca gttggtctat cggttttgca 1250
gtgtgtccga cgaatccaat gatctccttt accaatactg cgatgctgag 1300
tcaggctcca ccagttcggg ggtctatctg cgtctgaaag atccagacaa 1350
aaagaattgg aagcgcaaaa tcattgggt ctactcaggg caccagtggg 1400

tggatgtcca cgggggttcag aaggactaca acgttgctgt tcgcatcact 1450
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 ttgtgcttac ggctaacaga gacctgaaac agggcgggtgt atcatctaaa 1550
 tcacagagaa aaccagctct gcttaccgta gtgagatcac ttcataggtt 1600
 atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaaatca 1650
 ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700
 gtgggcactt caatgccaaag tatatactct tctttacatg gtgatgagtt 1750
 tcatttgtag aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800
 accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850
 ctcagggtcc tactctaaga agaatcta ataggatgctgg ttgtgtatta 1900
 aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950
 atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000
 ttacagtcac gccctcaatg ttatatattg gttatctgtt gggctctggga 2050
 catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100
 attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150
 caatgtgtat tatttaaaaa tgggagaaat agtttgttct atgaaataaa 2200
 cctagtttag aaatagggaa gctgagacat tttaagatct caagttttta 2250
 tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300
 cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500
 cctcaaaatg cctcaaaatg cctcaaaatg cctcaaaatg 2550

<210> 296

<211> 413

<212> PRT

<213> Homo sapiens

<400> 296

Met	Glu	Asn	Met	Leu	Leu	Trp	Leu	Ile	Phe	Phe	Thr	Pro	Gly	Trp
1				5				10					15	

Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His

	20	25	30
Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu	35	40	45
Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr	50	55	60
Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu	65	70	75
Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn	80	85	90
Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu	95	100	105
Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg	110	115	120
Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp	125	130	135
Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu	140	145	150
Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu	155	160	165
Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly	170	175	180
Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser	185	190	195
Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala	200	205	210
Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu	215	220	225
Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln	230	235	240
Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys	245		250
Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp	260	265	270
Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Ile Lys Arg Ala	275	280	285
His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys	290	295	300
Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp			

305	310	315
Arg Ala Asp Gln Leu Val Tyr Arg Phe	Cys Ser Val Ser Asp Glu	
320	325	330
Ser Asn Asp Leu Leu Tyr Gln Tyr Cys	Asp Ala Glu Ser Gly Ser	
335	340	345
Thr Gly Ser Gly Val Tyr Leu Arg Leu	Lys Asp Pro Asp Lys Lys	
350	355	360
Asn Trp Lys Arg Lys Ile Ile Ala Val	Tyr Ser Gly His Gln Trp	
365	370	375
Val Asp Val His Gly Val Gln Lys Asp	Tyr Asn Val Ala Val Arg	
380	385	390
Ile Thr Pro Leu Lys Tyr Ala Gln Ile	Cys Leu Trp Ile His Gly	
395	400	405
Asn Asp Ala Asn Cys Ala Tyr Gly		
410		

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacctgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 298

catggtccc gtgaatccag aggc 24

<210> 299

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 299

gaaggagggc cttcctttca gtggaccggg atcaagaata cccac 41

<210> 300

<211> 1869

<212> DNA

<213> Homo sapiens

<400> 300

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gcaactcctg gcacactgct cctctttctg gctttcctgc tectgagttc 200
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250
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ctgaggcgct gctgagcag caagagctgt gaaggaagaa atatccgata 350
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 gtttaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800
 taagtgaat catctacca aagctttttg gctctcaaat taaagattga 1850
 ttagtttcaa aaaaaaaaaa 1869

<210> 301

<211> 525

<212> PRT

<213> Homo sapiens

<400> 301

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Leu	Ala	Phe	Leu	Leu	Leu	Ser	Ser	Arg	Thr	Ala	Arg	Ser	Glu	Glu
			20						25					30
Asp	Arg	Asp	Gly	Leu	Trp	Asp	Ala	Trp	Gly	Pro	Trp	Ser	Glu	Cys
			35						40					45
Ser	Arg	Thr	Cys	Gly	Gly	Gly	Ala	Ser	Tyr	Ser	Leu	Arg	Arg	Cys
			50						55					60
Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr
			65						70					75
Gln	Gln	Gly	Leu	Asp	Lys	Phe	Ile	Gln	Ala	Ile	Arg	Arg	Arg	Ala
			80						85					90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe
			95						100					105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser
			110						115					120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala
			125						130					135

Pro Lys Val Leu Asp Gly Thr Arg Cys Tyr Thr Glu Ser Leu Asp	140	145	150
Met Cys Ile Ser Gly Leu Cys Gln Ile Val Gly Cys Asp His Gln	155	160	165
Leu Gly Ser Thr Val Lys Glu Asp Asn Cys Gly Val Cys Asn Gly	170	175	180
Asp Gly Ser Thr Cys Arg Leu Val Arg Gly Gln Tyr Lys Ser Gln	185	190	195
Leu Ser Ala Thr Lys Ser Asp Asp Thr Val Val Ala Leu Pro Tyr	200	205	210
Gly Ser Arg His Ile Arg Leu Val Leu Lys Gly Pro Asp His Leu	215	220	225
Tyr Leu Glu Thr Lys Thr Leu Gln Gly Thr Lys Gly Glu Asn Ser	230	235	240
Leu Ser Ser Thr Gly Thr Phe Leu Val Asp Asn Ser Ser Val Asp	245	250	255
Phe Gln Lys Phe Pro Asp Lys Glu Ile Leu Arg Met Ala Gly Pro	260	265	270
Leu Thr Ala Asp Phe Ile Val Lys Ile Arg Asn Ser Gly Ser Ala	275	280	285
Asp Ser Thr Val Gln Phe Ile Phe Tyr Gln Pro Ile Ile His Arg	290	295	300
Trp Arg Glu Thr Asp Phe Phe Pro Cys Ser Ala Thr Cys Gly Gly	305	310	315
Gly Tyr Gln Leu Thr Ser Ala Glu Cys Tyr Asp Leu Arg Ser Asn	320	325	330
Arg Val Val Ala Asp Gln Tyr Cys His Tyr Tyr Pro Glu Asn Ile	335	340	345
Lys Pro Lys Pro Lys Leu Gln Glu Cys Asn Leu Asp Pro Cys Pro	350	355	360
Ala Ser Asp Gly Tyr Tyr Gln Ile Met Pro Tyr Asp Leu Tyr His	365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro Trp Thr Ala Cys Ser Ser	380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg Ala Val Ser Cys Val Glu	395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser Val Glu Glu Trp Lys Cys	410	415	420

Met	Tyr	Thr	Pro	Lys	Met	Pro	Ile	Ala	Gln	Pro	Cys	Asn	Ile	Phe
				425					430					435
Asp	Cys	Pro	Lys	Trp	Leu	Ala	Gln	Glu	Trp	Ser	Pro	Cys	Thr	Val
				440					445					450
Thr	Cys	Gly	Gln	Gly	Leu	Arg	Tyr	Arg	Val	Val	Leu	Cys	Ile	Asp
				455					460					465
His	Arg	Gly	Met	His	Thr	Gly	Gly	Cys	Ser	Pro	Lys	Thr	Lys	Pro
				470					475					480
His	Ile	Lys	Glu	Glu	Cys	Ile	Val	Pro	Thr	Pro	Cys	Tyr	Lys	Pro
				485					490					495
Lys	Glu	Lys	Leu	Pro	Val	Glu	Ala	Lys	Leu	Pro	Trp	Phe	Lys	Gln
				500					505					510
Ala	Gln	Glu	Leu	Glu	Glu	Gly	Ala	Ala	Val	Ser	Glu	Glu	Pro	Ser
				515					520					525

<210> 302

<211> 1533

<212> DNA

<213> Homo sapiens

<400> 302

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ccagcggctg ccgagaggcg gggaccccg cctcatgcac gggaagactg 200
tgctgatcac cggggcgaac agcggcctgg gcgcgcacac ggccgcagag 250
ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300
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caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650
aatacggaga catcaatttt gatgaattga acagtgaaca aagctataat 700
aaaagctttt gttatagccg gagcaaaactg gctaacatto ttttaccag 750

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 aagtacaatg aaaaatacaa ttatattgta aaattataac tgggcaagca 1350
 tggatgacat attaatattt gtcagaatta agtgactcaa agtgcctatg 1400
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450
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 cacaagtctt acttgaata aatttactgg tac 1533

<210> 303

<211> 336

<212> PRT

<213> Homo sapiens

<400> 303

Met	Ala	Val	Ala	Thr	Ala	Ala	Ala	Val	Leu	Ala	Ala	Leu	Gly	Gly
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Ala	Leu	Trp	Leu	Ala	Ala	Arg	Arg	Phe	Val	Gly	Pro	Arg	Val	Gln
			20						25				30	

Arg	Leu	Arg	Arg	Gly	Gly	Asp	Pro	Gly	Leu	Met	His	Gly	Lys	Thr
				35					40				45	

Val	Leu	Ile	Ile	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala
				50					55				60	

Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg
				65					70				75	

Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu
				80					85				90	

Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	95	100	105
Val Gly Glu Leu Ile Val Arg Glu Leu Asp Leu Ala Ser Leu Arg	110	115	120
Ser Val Arg Ala Phe Cys Gln Glu Met Leu Gln Glu Glu Pro Arg	125	130	135
Leu Asp Val Leu Ile Asn Asn Ala Gly Ile Phe Gln Cys Pro Tyr	140	145	150
Met Lys Thr Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His	155	160	165
Leu Gly His Phe Leu Leu Thr Asn Leu Leu Leu Gly Leu Leu Lys	170	175	180
Ser Ser Ala Pro Ser Arg Ile Val Val Val Ser Ser Lys Leu Tyr	185	190	195
Lys Tyr Gly Asp Ile Asn Phe Asp Asp Leu Asn Ser Glu Gln Ser	200	205	210
Tyr Asn Lys Ser Phe Cys Tyr Ser Arg Ser Lys Leu Ala Asn Ile	215	220	225
Leu Phe Thr Arg Glu Leu Ala Arg Arg Leu Glu Gly Thr Asn Val	230	235	240
Thr Val Asn Val Leu His Pro Gly Ile Val Arg Thr Asn Leu Gly	245	250	255
Arg His Ile His Ile Pro Leu Leu Val Lys Pro Leu Phe Asn Leu	260	265	270
Val Ser Trp Ala Phe Phe Lys Thr Pro Val Glu Gly Ala Gln Thr	275	280	285
Ser Ile Tyr Leu Ala Ser Ser Pro Glu Val Glu Gly Val Ser Gly	290	295	300
Arg Tyr Phe Gly Asp Cys Lys Glu Glu Glu Leu Leu Pro Lys Ala	305	310	315
Met Asp Glu Ser Val Ala Arg Lys Leu Trp Asp Ile Ser Gln Val	320	325	330
Met Val Gly Leu Leu Lys	335		

<210> 304
 <211> 521
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure

<222> 20, 34, 62, 87, 221, 229
<223> unknown base

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gtgatcagga atggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200
tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250
actgaaaaat ttttttggg ataagagaat ttcagcaaag atgtttttaa 300
tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350
attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400
gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450
tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500
tggaaattat ctgcctgggt t 521

<210> 305
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 305
ccaggaaatg ctccaggaag agcc 24

<210> 306
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 306
accatgaca ccaaattgaa gaattca 26

<210> 307
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 307

aacgcaggga tcttccagtg cctttacatg aagactgaag atggg 45

<210> 308

<211> 1523

<212> DNA

<213> Homo sapiens

<400> 308

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ccagcgcttg tccctgtcac ggaccccagc gttaccatgc atcctgcctg 150
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aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309

<211> 406

<212> PRT

<213> Homo sapiens

<400> 309

Met	His	Pro	Ala	Val	Phe	Leu	Ser	Leu	Pro	Asp	Leu	Arg	Cys	Ser
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Leu	Leu	Leu	Leu	Val	Thr	Trp	Val	Phe	Thr	Pro	Val	Thr	Thr	Glu
				20				25					30	
Ile	Thr	Ser	Leu	Ala	Thr	Glu	Asn	Ile	Asp	Glu	Ile	Leu	Asn	Asn
				35				40					45	
Ala	Asp	Val	Ala	Leu	Val	Asn	Phe	Tyr	Ala	Asp	Trp	Cys	Arg	Phe
				50				55					60	
Ser	Gln	Met	Leu	His	Pro	Ile	Phe	Glu	Glu	Ala	Ser	Asp	Val	Ile
				65				70					75	
Lys	Glu	Glu	Phe	Pro	Asn	Glu	Asn	Gln	Val	Val	Phe	Ala	Arg	Val
				80				85					90	
Asp	Cys	Asp	Gln	His	Ser	Asp	Ile	Ala	Gln	Arg	Tyr	Arg	Ile	Ser
				95				100					105	
Lys	Tyr	Pro	Thr	Leu	Lys	Leu	Phe	Arg	Asn	Gly	Met	Met	Met	Lys
				110				115					120	
Arg	Glu	Tyr	Arg	Gly	Gln	Arg	Ser	Val	Lys	Ala	Leu	Ala	Asp	Tyr
				125				130					135	
Ile	Arg	Gln	Gln	Lys	Ser	Asp	Pro	Ile	Gln	Gln	Ile	Arg	Asp	Leu
				140				145					150	
Ala	Glu	Ile	Thr	Thr	Leu	Asp	Arg	Ser	Lys	Arg	Asn	Ile	Ile	Gly
				155				160					165	
Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170				175					180	
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185				190					195	

Gly Asp Val Ser Lys Pro Glu Arg Tyr Ser Gly Asp Asn Ile Ile	200	205	210
Tyr Lys Pro Pro Gly His Ser Ala Pro Asp Met Val Tyr Leu Gly	215	220	225
Ala Met Thr Asn Phe Asp Val Thr Tyr Asn Trp Ile Gln Asp Lys	230	235	240
Cys Val Pro Leu Val Arg Glu Ile Thr Phe Glu Asn Gly Glu Glu	245	250	255
Leu Thr Glu Glu Gly Leu Pro Phe Leu Ile Leu Phe His Met Lys	260	265	270
Glu Asp Thr Glu Ser Leu Glu Ile Phe Gln Asn Glu Val Ala Arg	275	280	285
Gln Leu Ile Ser Glu Lys Gly Thr Ile Asn Phe Leu His Ala Asp	290	295	300
Cys Asp Lys Phe Arg His Pro Leu Leu His Ile Gln Lys Thr Pro	305	310	315
Ala Asp Cys Pro Val Ile Ala Ile Asp Ser Phe Arg His Met Tyr	320	325	330
Val Phe Gly Asp Phe Lys Asp Val Leu Ile Pro Gly Lys Leu Lys	335	340	345
Gln Phe Val Phe Asp Leu His Ser Gly Lys Leu His Arg Glu Phe	350	355	360
His His Gly Pro Asp Pro Thr Asp Thr Ala Pro Gly Glu Gln Ala	365	370	375
Gln Asp Val Ala Ser Ser Pro Pro Glu Ser Ser Phe Gln Lys Leu	380	385	390
Ala Pro Ser Glu Tyr Arg Tyr Thr Leu Leu Arg Asp Arg Asp Glu	395	400	405

Leu

<210> 310

<211> 182

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 36, 48

<223> unknown base

<400> 310

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caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311
<211> 598
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396
<223> unknown base

<400> 311
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ccagcgctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200
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gggtttttac tctgttaaca actgaaataa cnngtcttga taennagaat 300
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tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400
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agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550
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<210> 312
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 312
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<210> 313
<211> 19
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 313

gtcagcgatc agtgaaagc 19

<210> 314

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 314

ccagaatgaa gtagctcggc 20

<210> 315

<211> 20

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<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 315

ccgaactcaaa atgcattgtc 20

<210> 316

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 316

catttggcag gaattgtcc 19

<210> 317

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 317

gggtgctatag gccaaagg 18

<210> 318

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgctcttcta tctttacccg acctcagatg ctcccttctg ctcttg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggcccttctgc tacatgctgg 50

cgctgctgct caatgcgcgc ctcatcttct tggccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcttatag accagtgtaa 150

tacctgaat ccccttgtag tcccagaqta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcacactgac ttacactggg tctcaatata 250

ccctctcttg catatcatat ttggacatat ttcaactata caatgatgaa 300

tggcccaqga ctctatgacc ctacaaccat catgaatgca gatattctag 350

catattgtca gaaggaagga tggatcaaat tagcttttta tcttttagaa 400

tttttttact acctatatgg catgatctat gttttgggtga gctcttagaa 450

caacacacag aagaattggg ccagtttaagt gcatgcaaaa agccacaaaa 500

tgaagggaat ctatcagaa aatctctgt caaactatga ctatggaata 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaaat gtttcacat 600

ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650
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 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050
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 ttttatttgt aagacattac ttattaagaa attgggttatt atgcttactg 1200
 ttctaacttg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322

<211> 144

<212> PRT

<213> Homo sapiens

<400> 322

Met	Ala	Phe	Thr	Phe	Ala	Ala	Phe	Cys	Tyr	Met	Leu	Ala	Leu	Leu
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Leu	Thr	Ala	Ala	Leu	Ile	Phe	Phe	Ala	Ile	Trp	His	Ile	Ile	Ala
				20					25				30	
Phe	Asp	Glu	Leu	Lys	Thr	Asp	Tyr	Lys	Asn	Pro	Ile	Asp	Gln	Cys
				35					40				45	
Asn	Thr	Leu	Asn	Pro	Leu	Val	Leu	Pro	Glu	Tyr	Leu	Ile	His	Ala
				50					55				60	
Phe	Phe	Cys	Val	Met	Phe	Leu	Cys	Ala	Ala	Glu	Trp	Leu	Thr	Leu
				65					70				75	
Gly	Leu	Asn	Met	Pro	Leu	Leu	Ala	Tyr	His	Ile	Trp	Arg	Tyr	Met
				80					85				90	
Ser	Arg	Pro	Val	Met	Ser	Gly	Pro	Gly	Leu	Tyr	Asp	Pro	Thr	Thr
				95					100				105	

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp
110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr
125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser
140

<210> 323

<211> 477

<212> DNA

<213> Homo sapiens

<400> 323

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tgtaataccc tgaatcccct tgtactccca gactacctca tccacgcttt 100
cttctgtgtc atgtttcttt gtgcagcaga gtggcttaca ctgggtctca 150
atatgcccct cttggcatat catatttgga ggtatatgag tagaccagtg 200
atgagtggcc caggactctc tgacctaca accatcatga atgcagatat 250
tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300
tagcattttt ttactacctc tatggcatga tctatgtttt ggtgagctct 350
tagaacaaca cacagaagaa ttgggtccagt taagtgcagc caaaaagcca 400
ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450
gaatctgata agttacttta aaaaatg 477

<210> 324

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 324

g a a a a g a c g g c a g t c a a t a g a t t c a a t a t t a a c t 43

<210> 325

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 325

c a g g a a a c a g c t a t g a c c a c c t g c a c a c c t g c a a a t c c a t t 41

<210> 326
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 326
gtgcagcaga gtggcttaca 20

<210> 327
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 327
actggaccaa ttctttctgtg 20

<210> 328
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 328
gatattctag catattgtca gaaggaagga tggcgcaaatt tagct 45

<210> 329
<211> 1174
<212> DNA
<213> Homo sapiens

<400> 329
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gagcccaact aggaatccca cccctccttc tctcaccat agccctggcc 150
agaagttccc agaccacttc agctdaagca tttagactgg tcttgggtga 200
tacggcctct taccaccagg cctgtcagtt gaactacccc ttgcacacct 250
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caagaacaac ttatgtccct gatgccaaaa atgcacctac tctttccctct 500
 aactctgggtg aggtcattct ggagtgacat gatggactcc gcacagagct 550
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 ttttaaaatg gtttcattgg atataggoot taagaaatca ctataaaatg 1150
 caaataaagt tactcaaac tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
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Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20					25					30	
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35					40					45	
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50					55					60	
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65					70					75	
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80					85					90	
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95					100					105	

Gln Ser Asp Glu Gln Tyr Ala Cys His Leu Gly Cys Gln Asn Gln	110	115	120
Leu Pro Phe Ala Glu Leu Arg Gln Glu Gln Leu Met Ser Leu Met	125	130	135
Pro Lys Met His Leu Leu Phe Pro Leu Thr Leu Val Arg Ser Phe	140	145	150
Trp Ser Asp Met Met Asp Ser Ala Gln Ser Phe Ile Thr Ser Ser	155	160	165
Trp Thr Phe Tyr Leu Gln Ala Asp Asp Gly Lys Ile Val Ile Phe	170	175	180
Gln Ser Lys Pro Glu Ile Gln Tyr Ala Pro His Leu Glu Gln Glu	185	190	195
Pro Thr Asn Leu Arg Glu Ser Ser Leu Ser Lys Met Ser Tyr Leu	200	205	210
Gln Met Arg Asn Ser Gln Ala His Arg Asn Phe Leu Glu Asp Gly	215	220	225
Glu Ser Asp Gly Phe Leu Arg Cys Leu Ser Leu Asn Ser Gly Trp	230	235	240
Ile Leu Thr Thr Thr Leu Val Leu Ser Val Met Val Leu Leu Trp	245	250	255
Ile Cys Cys Ala Thr Val Ala Thr Ala Val Glu Gln Tyr Val Pro	260	265	270
Ser Glu Lys Leu Ser Ile Tyr Gly Asp Leu Glu Phe Met Asn Glu	275	280	285
Gln Lys Leu Asn Arg Tyr Pro Ala Ser Ser Leu Val Val Val Arg	290	295	300
Ser Lys Thr Glu Asp His Glu Glu Ala Gly Pro Leu Pro Thr Lys	305	310	315
Val Asn Leu Ala His Ser Glu Ile	320		

<210> 331

<211> 310

<212> DNA

<213> Homo sapiens

<400> 331

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ggctgttttc aatttgtcag tttgtggatg atggaattga cttaaatcga 150

actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaatctga 200
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgctg 250
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<210> 332
 <211> 562
 <212> DNA
 <213> Homo sapiens

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 <221> unsure
 <222> 47
 <223> unknown base

<400> 332
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 aacagcaac aagctgagct gctgtgacag agggaaacaag atggcgqgcg 100
 tgaaggagc ctttgggtta gacccaaact ggggttccc cctgtgtgc 150
 tgcagaccat ggcttggcc ggaggttcgg ggaccgcttc ggcctgaagca 200
 tttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250
 gacctacccc ttgcacacct acctaaagga agaggagttg tacgcatgtc 300
 agagaggttg caggctgttt tcaatttgc agtttgtgga tgatggaatt 350
 gacttaaate gaactaaatt ggaatgtgaa tctgcatgta cagaagcata 400
 ttcacaatct gatgagcaat atgcttgcca tcttgggttc cagaatcagc 450
 tgcatttcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500
 atgcacctac tcttctctct aactctggtg aggtcattct ggagtgacat 550
 gatgactcc gc 562

<210> 333
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 333
 acaagctgag ctgctgtgac ag 22

<210> 334
 <211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 334
tgattctggc aaccaagatg gc 22

<210> 335
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 335
atggccttgg cgggaggttc ggggaccgct tcggctqaag 40

<210> 336
<211> 1885
<212> DNA
<213> Homo sapiens

<400> 336
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agggcgcacg gccgcgcacc gagcgtgcgg actggcctcc caagcgtggg 150
gggacaagct gccggagctg caatggggcg cggctgggga ttcttgtttg 200
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 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<100> 337
 <211> 468
 <212> PRT
 <213> Homo sapiens

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 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr
 20 25 30

Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp	35	40	45
Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg	50	55	60
Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg	65	70	75
Tyr Tyr Lys Val Asn Leu Lys Arg Pro Cys Pro Phe Trp Asn Asp	80	85	90
Ile Ser Gln Cys Gly Arg Arg Asp Cys Ala Val Lys Pro Cys Gln	95	100	105
Ser Asp Glu Val Pro Asp Gly Ile Lys Ser Ala Ser Tyr Lys Tyr	110	115	120
Ser Glu Glu Ala Asn Asn Leu Ile Glu Glu Cys Glu Gln Ala Glu	125	130	135
Arg Leu Gly Ala Val Asp Glu Ser Leu Ser Glu Glu Thr Gln Lys	140	145	150
Ala Val Leu Gln Trp Thr Lys His Asp Asp Ser Ser Asp Asn Phe	155	160	165
Cys Glu Ala Asp Asp Ile Gln Ser Pro Glu Ala Glu Tyr Val Asp	170	175	180
Leu Leu Leu Asn Pro Glu Arg Tyr Thr Gly Tyr Lys Gly Pro Asp	185	190	195
Ala Trp Lys Ile Trp Asn Val Ile Tyr Glu Glu Asn Cys Phe Lys	200	205	210
Pro Gln Thr Ile Lys Arg Pro Leu Asn Pro Leu Ala Ser Gly Gln	215	220	225
Gly Thr Ser Glu Glu Asn Thr Phe Tyr Ser Trp Leu Glu Gly Leu	230	235	240
Cys Val Glu Lys Arg Ala Phe Tyr Arg Leu Ile Ser Gly Leu Phe	245	250	255
Ala Ser Ile Asn Glu His Leu Ser Ala Arg Tyr Leu Leu Gln Glu	260	265	270
Thr Trp Leu Glu Lys Lys Trp Gly His Asn Ile Thr Glu Phe Gln	275	280	285
Gln Arg Phe Asp Gly Ile Leu Thr Glu Gly Glu Gly Pro Arg Arg	290	295	300
Leu Lys Asn Leu Tyr Phe Leu Tyr Leu Ile Glu Leu Arg Ala Leu	305	310	315

Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	320	325	330
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	335	340	345
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	350	355	360
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	365	370	375
Glu	Asp	Phe	Arg	Leu	His	Phe	Arg	Asn	Ile	Ser	Arg	Ile	Met	Asp	380	385	390
Cys	Val	Gly	Cys	Phe	Lys	Cys	Arg	Leu	Trp	Gly	Lys	Leu	Gln	Thr	395	400	405
Gln	Gly	Leu	Gly	Thr	Ala	Leu	Lys	Ile	Leu	Phe	Ser	Glu	Lys	Leu	410	415	420
Ile	Ala	Asn	Met	Pro	Glu	Ser	Gly	Pro	Ser	Tyr	Glu	Phe	His	Leu	425	430	435
Thr	Arg	Gln	Glu	Ile	Val	Ser	Leu	Phe	Asn	Ala	Phe	Gly	Arg	Ile	440	445	450
Ser	Thr	Ser	Val	Lys	Glu	Leu	Glu	Asn	Phe	Arg	Asn	Leu	Leu	Gln	455	460	465

Asn Ile His

<210> 338

<211> 507

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 101, 263, 376, 397, 426

<223> unknown base

<400> 338

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ctacagactt atatctgccc tacatgcaag cattaatgtg catttgagtg 200
caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaa 250
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<210> 339

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 339

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<210> 340

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 340

ttgcttctta atcctgagcg c 21

<210> 341

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 341

aaaggaggac ttctgactgc 20

<210> 342

<211> 26

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 342

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<210> 343

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 343

tgtccagaaa caggcacata tcagc 25

<210> 344

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

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<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

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ggactttctca tactggacag aaaccgatca ggcattggaac tccccttctg 150
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cctggccagg tgtggtggcc cacacgtga attctagcac tttgggaggg 1050
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<210> 346
<211> 124
<212> PRT
<213> Homo sapiens

<400> 346
Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe
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Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro
20 25 30
Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val
35 40 45
Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala
50 55 60
Met Arg Asp Gly Pro Ser Gly Asn Arg Arg Gly Asp Val Tyr Arg
65 70 75
Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His
80 85 90
Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn
95 100 105
Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly
110 115 120

Phe Met Val Ser

<210> 347
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 22
<223> unknown base

<400> 347
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ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100
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ggcatggaac tccccttctg cactcacctg ttcttgcccc tgggtgttct 200
cacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250
tcccagggcc accagaaagc aaatttggat acagtgctct acaacatgtt 300
gggggtggac agcgatggat gctgggtggg gccccctggg atggggccttc 350
aggcgaccgg aggggggacg tttatcgctg cctgtaggg gggggccaca 400
atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450
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tggtgatgg 509

<210> 348
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 348
ttttaggg gggaggggac ttc 23

<210> 349
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<221> Synthetic oligonucleotide probe

<400> 349
caggtgcata ttacagcag gatg 24

<210> 350
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 350
ggaactcccc ttcttcactc acctgttctt gcccctggtg ttctt 45

<210> 351
<211> 2056
<212> DNA
<213> Homo sapiens

<400> 351
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tcagctccaa catatgcatt ctgaagaaa atgctcaga tctcagaa 200
gctttatatt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250
tgcagacttt cacaatggtt ctagaagaaa tctggacaag tctttctatg 300
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 aattcagcaa ataaaaaggg ccacctggc caaaagcggg aaaaaaaaaa 2050
 aaaaaa 2056

<210> 350

<211> 311

<212> PR1

<213> Homo sapiens

<400> 352

Met	Gln	Thr	Phe	Thr	Met	Val	Leu	Glu	Glu	Ile	Trp	Thr	Ser	Leu
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Phe	Met	Trp	Phe	Phe	Tyr	Ala	Leu	Ile	Pro	Cys	Leu	Leu	Thr	Asp
					20				25					30

Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser	35	40	45
Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro	50	55	60
Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu	65	70	75
Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser	80	85	90
Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala	95	100	105
Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln	110	115	120
Thr Ser Ala Trp Ser Ile Leu Lys His Pro Phe Asn Arg Asn Ser	125	130	135
Thr Ile Leu Thr Arg Pro Gly Met Glu Ile Thr Lys Asp Gly Phe	140	145	150
His Leu Val Ile Glu Leu Glu Asp Leu Gly Pro Gln Phe Glu Phe	155	160	165
Leu Val Ala Tyr Trp Arg Arg Glu Pro Gly Ala Glu Glu His Val	170	175	180
Lys Met Val Arg Ser Gly Gly Ile Pro Val His Leu Glu Thr Met	185	190	195
Glu Pro Gly Ala Ala Tyr Cys Val Lys Ala Gln Thr Phe Val Lys	200	205	210
Ala Ile Gly Arg Tyr Ser Ala Phe Ser Gln Thr Glu Cys Val Glu	215	220	225
Val Gln Gly Glu Ala Ile Pro Leu Val Leu Ala Leu Phe Ala Phe	230	235	240
Val Gly Phe Met Leu Ile Leu Val Val Val Pro Leu Phe Val Trp	245	250	255
Lys Met Gly Arg Ala Leu Gln Tyr Ser Lys Cys Pro Val Val Val	260	265	270
Leu Pro Asp Thr Leu Lys Ile Thr Asn Ser Pro Gln Lys Leu Ile	275	280	285
Ser Cys Arg Arg Glu Glu Val Asp Ala Cys Ala Thr Ala Val Met	290	295	300
Ser Pro Glu Glu Leu Leu Arg Ala Trp Ile Ser	305	310	

<210> 353
<211> 864
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 654, 711, 748, 827
<223> unknown base

<400> 353
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tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150
agaatgcttt attttggaag gaaacaatgt tctaggtcaa actgagtcta 200
ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250
tcatgtggtt ttctacgca ttgattccat gtttgcacac agatgaagtg 300
gcattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350
gcattctctg atgtggagcc cagtgatgc gcctggagaa acagtgtact 400
attctgtcga ataccagggg gactacgaga gcctgtacac gagccacata 450
tggtatccca gcagctggtg ctcaactcact gaaggctctg agtgtgatgt 500
cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550
cattgggctc acagacctca gcctggagaa tctgaagca tccctttaat 600
agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650
cttnacactg gttattgagc tggaggacct ggggccccag tttgagttcc 700
ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750
gaaccccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800
taaccacat actcaatatg gacgaantgc tattctccac ctgtttgagt 850
gggctgggt tgat 864

<210> 354
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 354
aggttcgct ggcactagac ctc 23

<210> 355
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 355
ccaggtcggg taaggatggt tgag 24

<210> 356
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 356
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357
<211> 1670
<212> DNA
<213> Homo sapiens

<400> 357
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<210> 358

<211> 328

<212> PRT

<213> Homo sapiens

<214> 358

Met	Gly	Ala	Ala	Ala	Arg	Leu	Ser	Ala	Pro	Arg	Ala	Leu	Val	Leu
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Trp	Ala	Ala	Leu	Gly	Ala	Ala	Ala	His	Ile	Gly	Pro	Ala	Pro	Asp
			20						25				30	

Pro	Glu	Asp	Trp	Trp	Ser	Tyr	Lys	Asp	Asn	Leu	Gln	Gly	Asn	Phe
			35						40				45	

Val	Pro	Gly	Pro	Pro	Phe	Trp	Gly	Leu	Val	Asn	Ala	Ala	Trp	Ser
					50				55				60	

Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu	65	70	75
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser	80	85	90
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg	95	100	105
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser	110	115	120
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu	125	130	135
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn	140	145	150
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln	155	160	165
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly	170	175	180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn	185	190	195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile	200	205	210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu	215	220	225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser	230	235	240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile	245	250	255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg	260	265	270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser	275	280	285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg	290	295	300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro	305	310	315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg	320	325	

<210> 359

<211> 24

<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 359
tctgctgagg tgcagctcat tcac 24

<210> 360
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 360
gaggctctgg aagatctgag atgg 24

<210> 361
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 361
gectctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362
<211> 3038
<212> DNA
<213> Homo sapiens

<400> 362
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gcagctactg ctacagaaacg ctggggcgcc caccctggca gactaacgaa 150
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aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550
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 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363

<211> 500

<212> PRT

<213> Homo sapiens

<400> 363

Met	Lys	Cys	Thr	Ala	Arg	Glu	Trp	Leu	Arg	Val	Thr	Thr	Val	Leu
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Phe	Met	Ala	Arg	Ala	Ile	Pro	Ala	Met	Val	Val	Pro	Asn	Ala	Thr
				20				25					30	

Leu	Leu	Glu	Lys	Leu	Leu	Glu	Lys	Tyr	Met	Asp	Glu	Asp	Gly	Glu			
				35					40					45			
Trp	Trp	Ile	Ala	Lys	Gln	Arg	Gly	Lys	Arg	Ala	Ile	Thr	Asp	Asn			
				50					55					60			
Asp	Met	Gln	Ser	Ile	Leu	Asp	Leu	His	Asn	Lys	Leu	Arg	Ser	Gln			
				65					70					75			
Val	Tyr	Pro	Thr	Ala	Ser	Asn	Met	Glu	Tyr	Met	Thr	Trp	Asp	Val			
				80					85					90			
Glu	Leu	Glu	Arg	Ser	Ala	Glu	Ser	Trp	Ala	Glu	Ser	Cys	Leu	Trp			
				95					100					105			
Glu	His	Gly	Pro	Ala	Ser	Leu	Leu	Pro	Ser	Ile	Gly	Gln	Asn	Leu			
				110					115					120			
Gly	Ala	His	Trp	Gly	Arg	Tyr	Arg	Pro	Pro	Thr	Phe	His	Val	Gln			
				125					130					135			
Ser	Trp	Tyr	Asp	Glu	Val	Lys	Asp	Phe	Ser	Tyr	Pro	Tyr	Glu	His			
				140					145					150			
Glu	Cys	Asn	Pro	Tyr	Cys	Pro	Phe	Arg	Cys	Ser	Gly	Pro	Val	Cys			
				155					160					165			
Thr	His	Tyr	Thr	Gln	Val	Val	Trp	Ala	Thr	Ser	Asn	Arg	Ile	Gly			
				170					175					180			
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile			
				185					190					195			
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly			
				200					205					210			
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser			
				215					220					225			
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys			
				230					235					240			
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Gln			
				245					250					255			
Pro	Asn	Glu	Ile	Leu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His			
				260					265					270			
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser			
				275					280					285			
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg			
				290					295					300			
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala			
				305					310					315			

Gly Cys Leu Asp Ser Lys Ala Lys Val	Ile Gly Ser Val His Tyr
320	325 330
Glu Met Gln Ser Ser Ile Cys Arg Ala	Ala Ile His Tyr Gly Ile
335	340 345
Ile Asp Asn Asp Gly Gly Trp Val Asp	Ile Thr Arg Gln Gly Arg
350	355 360
Lys His Tyr Phe Ile Lys Ser Asn Arg	Asn Gly Ile Gln Thr Ile
365	370 375
Gly Lys Tyr Gln Ser Ala Asn Ser Phe	Thr Val Ser Lys Val Thr
380	385 390
Val Gln Ala Val Thr Cys Glu Thr Thr	Val Glu Gln Leu Cys Pro
395	400 405
Phe His Lys Pro Ala Ser His Cys Pro	Arg Val Tyr Cys Pro Arg
410	415 420
Asn Cys Met Gln Ala Asn Pro His Tyr	Ala Arg Val Ile Gly Thr
425	430 435
Arg Val Tyr Ser Asp Leu Ser Ser Ile	Cys Arg Ala Ala Val His
440	445 450
Ala Gly Val Val Arg Asn His Gly Gly	Tyr Val Asp Val Met Pro
455	460 465
Val Asp Lys Arg Lys Thr Tyr Ile Ala	Ser Phe Gln Asn Gly Ile
470	475 480
Phe Ser Glu Ser Leu Gln Asn Pro Pro	Gly Gly Lys Ala Phe Arg
485	490 495
Val Phe Ala Val Val	
500	

<210> 364

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

100 364

ggacagaatt tgggagcaca ctgg 24

<210> 365

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 365
ccaagagtat actgtcctcg 20

<210> 366
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 366
agcacagatt ttctctacag ccccc 25

<210> 367
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<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 367
ctccactcca gcatatactt ctac 24

<210> 368
<211> 50
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 368
ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369
<211> 1685
<212> DNA
<213> Homo sapiens

<400> 369
acqaaagaaa gggagagagc cagcgcacgg ccacagacag ccttgggcat 50
ccacgcagcg ggcagcggga ggcagcagag ccggaagggc cgcgcggggc 100
agagaaagcc gaggagagct ggggtggcgtc tccggggcgc cgtccgcagc 150
ggccagcgcc ctccccatgt cctgtctccc acgcgcgcgc cctccgggtc 200
gcatgaggct cctggcgggc gcgctgctcc tgtctgtgtt ggcgctgtac 250
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gatccgctac agcgacgtga agaagctgga aatgaagcca aagtaccgcg 350

actgcgagga gaagatgggt atcatcacca ccaagagcgt gtccagggtac 400
 cgagggtcagg agcactgcct gcaccccaag ctgcagagca ccaagcgctt 450
 catcaagtgg tacaacgcct ggaacgagaa ggcgagggtc tacgaagaat 500
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<210> 370

<211> 111

<212> PRT

<213> Homo sapiens

<400> 370

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Leu	Ala	Ala	Ala	Leu	Leu	Leu	Leu	Leu	Ala	Leu	Tyr	Thr	Ala
				20					25				30

Arg	Val	Asp	Gly	Ser	Lys	Cys	Lys	Cys	Ser	Arg	Lys	Gly	Pro	Lys
				35					40					45

Ile	Arg	Tyr	Ser	Asp	Val	Lys	Lys	Leu	Glu	Met	Lys	Pro	Lys	Tyr
				50					55					60

Pro	His	Cys	Glu	Glu	Lys	Met	Val	Ile	Ile	Thr	Thr	Lys	Ser	Val
				65					70					75

Ser	Arg	Tyr	Arg	Gly	Gln	Glu	His	Cys	Leu	His	Pro	Lys	Leu	Gln
				80					85					90

Ser	Thr	Lys	Arg	Phe	Ile	Lys	Trp	Tyr	Asn	Ala	Trp	Asn	Glu	Lys
				95					100					105

Arg	Arg	Val	Tyr	Glu	Glu
				110	

<210> 371

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

ccagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

ccccacctgg caggagatt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373
ctccggtcag catgaggctc ctggcggecg ctgctcctgc tgetg 45

<210> 374
<211> 3113
<212> DNA
<213> Homo sapiens

<400> 374
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acctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150
caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200
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gtaatgaccg tggatgaagc gaagatattc atgatcagaa cagtaagaag 550
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 taagagactt tgt 3113

<210> 375
 <211> 816
 <212> PRT
 <213> Homo sapiens

<400> 375
 Met Leu Asn Ser Asn Val Leu Leu Trp Leu Thr Ala Leu Ala Ile
 1 5 10 15
 Lys Phe Thr Leu Ile Asp Ser Gln Ala Gln Tyr Pro Val Val Asn
 20 25 30
 Thr Asn Tyr Gly Lys Ile Arg Gly Leu Arg Thr Pro Leu Pro Asn
 35 40 45
 Glu Ile Leu Gly Pro Val Glu Gln Tyr Leu Gly Val Pro Tyr Ala
 50 55 60
 Ser Pro Pro Thr Gly Glu Arg Arg Phe Gln Pro Pro Glu Pro Pro
 65 70 75
 Ser Ser Trp Thr Gly Ile Arg Asn Thr Thr Gln Phe Ala Ala Val
 80 85 90
 Lys Pro Gln His Leu Asp Glu Arg Ser Leu Leu His Asp Met Leu
 95 100
 Pro Ile Trp Phe Thr Ala Asn Leu Asp Thr Leu Met Thr Tyr Val
 110 115 120
 Gln Asp Gln Asn Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Val Pro
 125 130 135
 Thr Glu Asp Gly Ala Asn Thr Lys Lys Asn Ala Asp Asp Ile Thr
 140 145 150

Ser Asn Asp Arg Gly Glu Asp Glu Asp Ile His Asp Gln Asn Ser	155	160	165
Lys Lys Pro Val Met Val Tyr Ile His Gly Gly Ser Tyr Met Glu	170	175	180
Gly Thr Gly Asn Met Ile Asp Gly Ser Ile Leu Ala Ser Tyr Gly	185	190	195
Asn Val Ile Val Ile Thr Ile Asn Tyr Arg Leu Gly Ile Leu Gly	200	205	210
Phe Leu Ser Thr Gly Asp Gln Ala Ala Lys Gly Asn Tyr Gly Leu	215	220	225
Leu Asp Gln Ile Gln Ala Leu Arg Trp Ile Glu Glu Asn Val Gly	230	235	240
Ala Phe Gly Gly Asp Pro Lys Arg Val Thr Ile Phe Gly Ser Gly	245	250	255
Ala Gly Ala Ser Cys Val Ser Leu Leu Thr Leu Ser His Tyr Ser	260	265	270
Glu Gly Leu Phe Gln Lys Ala Ile Ile Gln Ser Gly Thr Ala Leu	275	280	285
Ser Ser Trp Ala Val Asn Tyr Gln Pro Ala Lys Tyr Thr Arg Ile	290	295	300
Leu Ala Asp Lys Val Gly Cys Asn Met Leu Asp Thr Thr Asp Met	305	310	315
Val Glu Cys Leu Arg Asn Lys Asn Tyr Lys Glu Leu Ile Gln Gln	320	325	330
Thr Ile Thr Pro Ala Thr Tyr His Ile Ala Phe Gly Pro Val Ile	335	340	345
Asp Gly Asp Val Ile Pro Asp Asp Pro Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu Asn Tyr Asp Ile Met Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys Phe Val Asp Gly Ile Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn Asp Phe Asp Phe Ser Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly Tyr Pro Glu Gly Lys Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met Tyr Thr Asp Trp Ala Asp Lys Glu Asn Pro Glu	425	430	435

Thr Arg Arg Lys Thr Leu Val Ala Leu Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala Val Ala Ala Asp Leu His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe Tyr Ala Phe Tyr His His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp Ala Asp Ser Ala His Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile Pro Met Ile Gly Pro Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys Asn Asp Val Met Leu Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn Phe Ala Lys Thr Gly Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr Lys Phe Ile His Thr Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp Ser Lys Tyr Asn Pro Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu Lys Pro Arg Val Arg Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe Trp Leu Glu Leu Val Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe Gln Tyr Val Ser Thr Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr Ser Phe Pro Tyr Gly Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro Thr Thr Lys Arg Pro Ala Ile Thr Pro Ala Asn	635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp	650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu	665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile	680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His	695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp	710	715	720

Ile	Ala	His	Ile	Gln	Asn	Glu	Glu	Ile	Met	Ser	Leu	Gln	Met	Lys
				725					730					735
Gln	Leu	Glu	His	Asp	His	Glu	Cys	Glu	Ser	Leu	Gln	Ala	His	Asp
				740					745					750
Thr	Leu	Arg	Leu	Thr	Cys	Pro	Pro	Asp	Tyr	Thr	Leu	Thr	Leu	Arg
				755					760					765
Arg	Ser	Pro	Asp	Asp	Ile	Pro	Leu	Met	Thr	Pro	Asn	Thr	Ile	Thr
				770					775					780
Met	Ile	Pro	Asn	Thr	Leu	Thr	Gly	Met	Gln	Pro	Leu	His	Thr	Phe
				785					790					795
Asn	Thr	Phe	Ser	Gly	Gly	Gln	Asn	Ser	Thr	Asn	Leu	Pro	His	Gly
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His	Ser	Thr	Thr	Arg	Val									
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<210> 376
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 376
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 377
 aacccccgag ccaaaagatg gtcac 25

<210> 378
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 378
 gtaccgggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379
 <211> 2461
 <212> DNA

<213> Homo sapiens

<400> 379

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 <211> 348
 <212> PRT
 <213> Homo sapiens

<400> 380
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				35					40					45			
Gln	Thr	Phe	Glu	Tyr	Leu	Lys	Arg	Glu	His	Ser	Leu	Ser	Lys	Pro			
				50					55					60			
Tyr	Gln	Gly	Val	Gly	Thr	Gly	Ser	Ser	Ser	Leu	Trp	Asn	Leu	Met			
				65					70					75			
Gly	Asn	Ala	Met	Val	Met	Thr	Gln	Tyr	Ile	Arg	Leu	Thr	Pro	Asp			
				80					85					90			
Met	Gln	Ser	Lys	Gln	Gly	Ala	Leu	Trp	Asn	Arg	Val	Pro	Cys	Phe			
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Leu	Arg	Asp	Trp	Glu	Leu	Gln	Val	His	Phe	Lys	Ile	His	Gly	Gln			
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Gly	Lys	Lys	Asn	Leu	His	Gly	Asp	Gly	Leu	Ala	Ile	Trp	Tyr	Thr			
				125					130					135			
Lys	Asp	Arg	Met	Gln	Pro	Gly	Pro	Val	Phe	Gly	Asn	Met	Asp	Lys			
				140					145					150			
Phe	Val	Gly	Leu	Gly	Val	Phe	Val	Asp	Thr	Tyr	Pro	Asn	Glu	Glu			
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Lys	Gln	Gln	Glu	Arg	Val	Phe	Pro	Tyr	Ile	Ser	Ala	Met	Val	Asn			
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Asn	Gly	Ser	Leu	Ser	Tyr	Asp	His	Glu	Arg	Asp	Gly	Arg	Pro	Thr			
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Glu	Leu	Gly	Gly	Cys	Thr	Ala	Ile	Val	Arg	Asn	Leu	His	Tyr	Asp			
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Thr	Phe	Leu	Val	Ile	Arg	Tyr	Val	Lys	Arg	His	Leu	Thr	Ile	Met			
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Met	Asp	Ile	Asp	Gly	Lys	His	Glu	Trp	Arg	Asp	Cys	Ile	Glu	Val			
				230					235					240			
Pro	Gly	Val	Arg	Leu	Pro	Arg	Gly	Tyr	Tyr	Phe	Gly	Thr	Ser	Ser			
				245					250					255			
Ile	Thr	Gly	Asp	Leu	Ser	Asp	Asn	His	Arg	Val	Ile	Gln	Leu	Lys			
				260					265					270			
Leu	Phe	Glu	Leu	Thr	Val	Glu	Arg	Thr	Pro	Glu	Glu	Glu	Lys	Leu			
				275					280					285			
His	Arg	Asp	Val	Phe	Leu	Pro	Ser	Val	Asp	Asn	Met	Lys	Leu	Pro			
				290					295					300			
Glu	Met	Thr	Ala	Pro	Leu	Pro	Pro	Leu	Ser	Gly	Leu	Ala	Leu	Phe			
				305					310					315			

Leu Ile Val Phe Phe Ser Leu Val Phe Ser Val Phe Ala Ile Val
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Ile Gly Ile Ile Leu Tyr Asn Lys Trp Gln Glu Gln Ser Arg Lys
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Arg Phe Tyr

<210> 381

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 381

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<210> 382

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 382

caactctccag gctgcatgct cagg 24

<210> 383

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 383

gtcaaacggt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384

<211> 2050

<212> DNA

<213> Homo sapiens

<400> 384

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ggggactcca agatttccat gaaqaaaatc agttgtcttc attcaagaat 150

tggggtctgg ctcaaatc ctgcagctgg tgaaaatctg tttctagaa 200

gaggtttaat taatgcctgc agtetgacat gttcccgatt tgaggtgaaa 250
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<210> 385

<211> 480

<212> PRT

<213> Homo sapiens

<400> 385

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Leu	Leu	Ala	Phe	Val	Ser	Leu	Ser	Leu	Gln	Phe	Phe	His	Leu	Ile
				20					25				30	

Pro	Val	Ser	Thr	Pro	Lys	Asn	Gly	Met	Ser	Ser	Lys	Ser	Arg	Lys
				35					40				45	

Arg	Ile	Met	Pro	Asp	Pro	Val	Thr	Glu	Pro	Pro	Val	Thr	Asp	Pro
				50					55				60	

Val	Tyr	Glu	Ala	Leu	Leu	Tyr	Cys	Asn	Ile	Pro	Ser	Val	Ala	Glu
				65					70					75

Arg	Ser	Met	Glu	Gly	His	Ala	Pro	His	His	Phe	Lys	Leu	Val	Ser
				80					85					90

Val	His	Val	Phe	Ile	Arg	His	Gly	Asp	Arg	Tyr	Pro	Leu	Tyr	Val
				95					100					105

Ile	Pro	Lys	Thr	Lys	Arg	Pro	Glu	Ile	Asp	Cys	Thr	Leu	Val	Ala
				110					115					120

Asn	Arg	Lys	Pro	Tyr	His	Pro	Lys	Leu	Glu	Ala	Phe	Ile	Ser	His
				125					130					135

Met	Ser	Lys	Gly	Ser	Gly	Ala	Ser	Phe	Glu	Ser	Pro	Leu	Asn	Ser
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Leu	Pro	Leu	Tyr	Pro	Asn	His	Pro	Leu	Cys	Glu	Met	Gly	Glu	Leu
				155					160					165

Thr	Gln	Thr	Gly	Val	Val	Gln	His	Leu	Gln	Asn	Gly	Gln	Leu	Leu
				170					175					180

Arg	Arg	Thr	Tyr	Val	Tyr	Tyr	Phe	Gly	Leu	Leu	Val	Leu	Asp	Arg
				185					190					195

Ser	Ala	Asp	Gln	Leu	Tyr	Leu	Glu	Thr	Thr	Gly	Lys	Ser	Arg	Thr
				200					205					210

Leu	Gln	Ser	Gly	Leu	Ala	Leu	Leu	Tyr	Gly	Phe	Leu	Pro	Asp	Phe
				215					220					225

Asp	Trp	Lys	Lys	Ile	Tyr	Phe	Arg	His	Gln	Pro	Ser	Ala	Leu	Phe
				230					235					240

Cys Ser Gly Ser Cys Tyr Cys Pro Val Arg Asn Gln Tyr Leu Glu	245	250	255
Lys Glu Gln Arg Arg Gln Tyr Leu Leu Arg Leu Lys Asn Ser Gln	260	265	270
Leu Glu Lys Thr Tyr Gly Glu Met Ala Lys Ile Val Asp Val Pro	275	280	285
Thr Lys Gln Leu Arg Ala Ala Asn Pro Ile Asp Ser Met Leu Cys	290	295	300
His Phe Cys His Asn Val Ser Phe Pro Cys Thr Arg Asn Gly Cys	305	310	315
Val Asp Met Glu His Phe Lys Val Ile Lys Thr His Gln Ile Glu	320	325	330
Asp Glu Arg Glu Arg Arg Glu Lys Lys Leu Tyr Phe Gly Tyr Ser	335	340	345
Leu Leu Gly Ala His Pro Ile Leu Asn Gln Thr Ile Gly Arg Met	350	355	360
Gln Arg Ala Thr Glu Gly Arg Lys Glu Glu Leu Phe Ala Leu Tyr	365	370	375
Ser Ala His Asp Val Thr Leu Ser Pro Val Leu Ser Ala Leu Gly	380	385	390
Leu Ser Glu Ala Arg Phe Pro Arg Phe Ala Ala Arg Leu Ile Phe	395	400	405
Glu Leu Trp Gln Asp Arg Glu Lys Pro Ser Glu His Ser Val Arg	410	415	420
Ile Leu Tyr Asn Gly Val Asp Val Thr Phe His Thr Ser Phe Cys	425	430	435
Gln Asp His His Lys Arg Ser Pro Lys Pro Met Cys Pro Leu Glu	440	445	450
Asn Leu Val Arg Phe Val Lys Arg Asp Met Phe Val Ala Leu Gly	455	460	465
Gly Ser Gly Thr Asn Tyr Tyr Asn Ala Cys His Arg Gln Gly Phe	470	475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 386

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<210> 387

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 387

ttccctatgc tctgtattgg catgg 25

<210> 388

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 388

gccacttctg ccacaatgtc agctttccct qtaccagaaa tggctgtgtt 50

<210> 389

<211> 3313

<212> DNA

<213> Homo sapiens

<400> 389

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gcccgtgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200

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gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300

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aattctggag gaagatcaga ctgattcctg cgggactgca cgggactac 400

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 <211> 916
 <212> PRT
 <213> Homo sapiens

<400> 390

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Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln			
			20						25					30			
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val			
			35						40					45			
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala			
			50						55					60			
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe			
			65						70					75			
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile			
			80						85					90			
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn			
			95						100					105			
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu			
			110						115					120			
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Gln			
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Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met			
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Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn			
			155						160					165			
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu			
			170						175					180			
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val			
			185						190					195			
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu			
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Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Ala	Thr	Gly	Thr			
			215						220					225			
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro			
			230						235					240			
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu			
			245						250					255			
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp			
			260						265					270			
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp			
			275						280					285			

Asp Lys Ala Ala Gln Val Phe Lys Leu	Asp Cys Asn Ser Gly Thr	290	295	300
Ile Ser Thr Ile Gly Glu Leu Asp His	Glu Glu Ser Gly Phe Tyr	305	310	315
Gln Met Glu Val Gln Ala Met Asp Asn	Ala Gly Tyr Ser Ala Arg	320	325	330
Ala Lys Val Leu Ile Thr Val Leu Asp	Val Asn Asp Asn Ala Pro	335	340	345
Glu Val Val Leu Thr Ser Leu Ala Ser	Ser Val Pro Glu Asn Ser	350	355	360
Pro Arg Gly Thr Leu Ile Ala Leu Leu	Asn Val Asn Asp Gln Asp	365	370	375
Ser Glu Glu Asn Gly Gln Val Ile Cys	Phe Ile Gln Gly Asn Leu	380	385	390
Pro Phe Lys Leu Glu Lys Ser Tyr Gly	Asn Tyr Tyr Ser Leu Val	395	400	405
Thr Asp Ile Val Leu Asp Arg Glu Gln	Val Pro Ser Tyr Asn Ile	410	415	420
Thr Val Thr Ala Thr Asp Arg Gly Thr	Pro Pro Leu Ser Thr Glu	425	430	435
Thr His Ile Ser Leu Asn Val Ala Asp	Thr Asn Asp Asn Pro Pro	440	445	450
Val Phe Pro Gln Ala Ser Tyr Ser Ala	Tyr Ile Pro Glu Asn Asn	455	460	465
Pro Arg Gly Val Ser Leu Val Ser Val	Thr Ala His Asp Pro Asp	470	475	480
Cys Glu Glu Asn Ala Gln Ile Thr Tyr	Ser Leu Ala Glu Asn Thr	485	490	495
Ile Gln Gly Ala Ser Leu Ser Ser Tyr	Val Ser Ile Asn Ser Asp	500	505	510
Thr Gly Val Leu Tyr Ala Leu Ser Ser	Ile Asp Tyr Glu Gln Phe	515	520	525
Arg Asp Leu Gln Val Lys Val Met Ala	Arg Asp Asn Gly His Pro	530	535	540
Pro Leu Ser Ser Asn Val Ser Leu Ser	Leu Phe Val Leu Asp Gln	545	550	555
Asn Asp Asn Ala Pro Glu Ile Leu Tyr	Pro Ala Leu Pro Thr Asp	560	565	570

Gly Ser Thr Gly Val Glu Leu Ala Pro Arg Ser Ala Glu Pro Gly	575	580	585
Tyr Leu Val Thr Lys Val Val Ala Val Asp Arg Asp Ser Gly Gln	590	595	600
Asn Ala Trp Leu Ser Tyr Arg Leu Leu Lys Ala Ser Glu Pro Gly	605	610	615
Leu Phe Ser Val Gly Leu His Thr Gly Glu Val Arg Thr Ala Arg	620	625	630
Ala Leu Leu Asp Arg Asp Ala Leu Lys Gln Ser Leu Val Val Ala	635	640	645
Val Gln Asp His Gly Gln Pro Pro Leu Ser Ala Thr Val Thr Leu	650	655	660
Thr Val Ala Val Ala Asp Ser Ile Pro Gln Val Leu Ala Asp Leu	665	670	675
Gly Ser Leu Glu Ser Pro Ala Asn Ser Glu Thr Ser Asp Leu Thr	680	685	690
Leu Tyr Leu Val Val Ala Val Ala Ala Val Ser Cys Val Phe Leu	695	700	705
Ala Phe Val Ile Leu Leu Leu Ala Leu Arg Leu Arg Arg Trp His	710	715	720
Lys Ser Arg Leu Leu Gln Ala Ser Gly Gly Gly Leu Thr Gly Ala	725	730	735
Pro Ala Ser His Phe Val Gly Val Asp Gly Val Gln Ala Phe Leu	740	745	750
Gln Thr Tyr Ser His Glu Val Ser Leu Thr Thr Asp Ser Arg Lys	755	760	765
Ser His Leu Ile Phe Pro Gln Pro Asn Tyr Ala Asp Met Leu Val	770	775	780
Ser Gln Glu Ser Phe Glu Lys Ser Glu Pro Leu Leu Leu Ser Gly	785	790	795
Asp Ser Val Phe Ser Lys Asp Ser His Gly Leu Ile Glu Val Ser	800	805	810
Leu Tyr Gln Ile Phe Phe Leu Phe Phe Phe Asn Cys Ser Val Ser	815	820	825
Gln Ala Gly Val Gln Arg Tyr Asp His Ser Ser Leu Arg Pro Gln	830	835	840
Thr Pro Arg Leu Lys Gln Leu Ser His Leu Cys Leu Arg Cys Asn	845	850	855

Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr
				860					865					870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu
				875					880					885
Ser	Cys	Thr	Asp	Gly	Ser	Leu	Thr	Pro	Val	Ile	Pro	Val	Leu	Trp
				890					895					900
Glu	Ala	Glu	Ala	Gly	Gly	Ser	Pro	Glu	Val	Gly	Ser	Leu	Arg	Pro
				905					910					915

Ala

<210> 391

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 391

ttcgtctctg tgaacggcc cac 23

<210> 392

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 392

ctcggggcgca ttgtcgttct ggta 24

<210> 393

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 393

ccactctaga cagagcag agcttca ctggtctcct 4

<210> 394

<211> 999

<212> DNA

<213> Homo sapiens

<400> 394

cccagggtct agtgcaggag gagaaggagg aggaacagga ggtggagatt 50

cccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100

ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150
 ctggaagacc tcaccatggg acgccccga cctcgtgogg ccaagacgtg 200
 gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250
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 caagaaatac ctgtggttca gtccatccca caccctgtgt acaacagcag 500
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 tccccagaaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750
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 gtcagacccc ctgtgggagg tccgacaaac ctggcgtcta taccaacata 900
 tgcgcctacc tggactggat caagaagata ataggcagca agggctgatt 950
 ctaggataag cactagatct cccctaataa actcacaact ctctgggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1														15

Leu	Leu	Leu	Gly	Gly	Ala	Thr	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30

Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
				35					40					45

Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
				50					55					60

Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
				65					70					75

Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	80	85	90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	95	100	105
His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396

<211> 24

<212> RNA

<213> Artificial Sequence

<220>

<221> Synthetic nucleotide sequence

<222> 396

gagctacag aataaagatg gcc 24

<210> 397

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 397

ggtgcaatga ttgcccagga tgat 24

<210> 398

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccataccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccgggtg caccggggggg gctgagcgcc tcttgcggcc cggcctgcgc 50
gtcccgagccc gcgcgcggcc ccacccccca acccgagccc ggcgcgccta 100
gcccccgccc gggcccgccc ccgcgcggcc gccaggtga gcgctccgcc 150
cgccgcgagg ccccgccccg gcccgcccc gcccgcccc ggcggcgggg 200
ggaacggggc ggattctctg cgcgtcaaac cactgatcc cataaaacat 250
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gcgcgcctcg cctgtgcgc cctgcgcgc ctgcgcaccc gcgggcgcag 350
ccagagccaga gccgggggga ggcggagcgg ccgagcctcg tcccgcggcc 400
gggcgggggc cgggcggtag cggcgggccc tggatgcgga cccggccgcg 450
gggagacggg cgcgcgcgcc gaaacgaatt tcagtccccg accgcgcgcc 500
cccaacccct agcatgaaga ggcgcgcgcc tgcgcgcgc cgcgcgcgc 550
catcctcctt atcctcctcct cctcctcctt tgcgcgcgc cgcgcgcgc 600
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 ttacagggtt cggcggcagc gtttgttcca gaacgcgcgc tcccaccag 2150
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met	Lys	Arg	Ala	Ser	Ala	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val
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Leu	Trp	Leu	Gln	Ala	Trp	Gln	Val	Ala	Ala	Pro	Cys	Pro	Gly	Ala
			20						25					30
Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln
				35					40					45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln
			50						55					60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala
				65					70					75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser
				80					85					90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala
				95					100					105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser
				110					115					120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu
				125					130					135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe
				140					145					150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala
				155					160					165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu
				170					175					180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu
				185					190					195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His
				200					205					210
Gln	Asn	Arg	Val	Ala	Phe	Thr	His	Phe	His	Ala	Leu	Arg	Asp	Leu
				215					220					225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala
				230					235					240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu
				245					250					255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro
				260					265					270

Leu Trp Ala Trp	Leu Gln Lys Phe Arg	Gly Ser Ser Ser Glu Val
275	280	285
Pro Cys Ser Leu	Pro Gln Arg Leu Ala	Gly Arg Asp Leu Lys Arg
290	295	300
Leu Ala Ala Asn Asp	Leu Gln Gly Cys Ala Val Ala Thr Gly Pro	
305	310	315
Tyr His Pro Ile Trp	Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu	
320	325	330
Gly Leu Pro Lys Cys	Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser	
335	340	345
Val Leu Glu Pro Gly	Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys	
350	355	360
Gly Arg Val Pro Pro	Gly Asp Ser Pro Pro Gly Asn Gly Ser Gly	
365	370	375
Pro Arg His Ile Asn	Asp Ser Pro Phe Gly Thr Leu Pro Gly Ser	
380	385	390
Ala Glu Pro Pro Leu	Thr Ala Val Arg Pro Glu Gly Ser Glu Pro	
395	400	405
Pro Gly Phe Pro Thr	Ser Gly Pro Arg Arg Arg Pro Gly Cys Ser	
410	415	420
Arg Lys Asn Arg Thr	Arg Ser His Cys Arg Leu Gly Gln Ala Gly	
425	430	435
Ser Gly Gly Gly Gly	Thr Gly Asp Ser Glu Gly Ser Gly Ala Leu	
440	445	450
Pro Ser Leu Thr Cys	Ser Leu Thr Pro Leu Gly Leu Ala Leu Val	
455	460	465
Leu Trp Thr Val Leu	Gly Pro Cys	
470		

<210> 401

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 401

tggtgcct gcagtacctc tacc 24

<210> 402

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<213> Synthetic oligonucleotide probe

<400> 402

cctgcaggt cattggcagc tagg 24

<210> 403

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150
agetgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200
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<210> 405

<211> 798

<212> PRT

<213> Homo sapiens

<400> 405

Met	Glu	Ala	Ser	Gly	Lys	Leu	Ile	Cys	Arg	Gln	Arg	Gln	Val	Leu
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Phe	Ser	Phe	Leu	Leu	Leu	Gly	Leu	Ser	Leu	Ala	Gly	Ala	Ala	Glu
			20						25					30
Pro	Arg	Ser	Tyr	Ser	Val	Val	Glu	Glu	Thr	Glu	Gly	Ser	Ser	Phe
			35						40					45
Val	Thr	Asn	Leu	Ala	Lys	Asp	Leu	Gly	Leu	Glu	Gln	Arg	Glu	Phe
			50						55					60
Ser	Arg	Arg	Gly	Val	Arg	Val	Val	Ser	Arg	Gly	Asn	Lys	Leu	His
			65						70					75
Leu	Gln	Leu	Asn	Gln	Gln	Thr	Ala	Asp	Leu	Leu	Leu	Asn	Glu	Lys
			80						85					90
Leu	Asp	Arg	Glu	Asp	Leu	Cys	Gly	His	Thr	Glu	Pro	Cys	Val	Leu
			95						100					105
Arg	Phe	Gln	Val	Leu	Leu	Glu	Ser	Pro	Phe	Glu	Phe	Phe	Gln	Ala
			110						115					120
Glu	Leu	Gln	Val	Ile	Asp	Ile	Asn	Asp	His	Ser	Pro	Val	Phe	Leu
			125						130					135
Asp	Lys	Gln	Met	Leu	Val	Lys	Val	Ser	Glu	Ser	Ser	Pro	Pro	Gly
			140						145					150

Thr Thr Phe Pro	Leu Lys Asn Ala Glu Asp	Leu Asp Val Gly Gln
	155	160 165
Asn Asn Ile Glu	Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg	
	170	175 180
Val Leu Thr Arg	Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu	
	185	190 195
Val Leu Asp Lys	Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg	
	200	205 210
Leu Thr Leu Thr	Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly	
	215	220 225
Thr Ala Gln Val	Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala	
	230	235 240
Pro Glu Phe Glu	Gln Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	
	245	250 255
Ser Pro Val Gly	Phe Leu Val Val Lys Val Ser Ala Thr Asp Val	
	260	265 270
Asp Thr Gly Val	Asn Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	
	275	280 285
Ser Glu Glu Ile	Gly Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	
	290	295 300
Glu Ile Glu Leu	Lys Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	
	305	310 315
Tyr Glu Val Asn	Ile Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	
	320	325 330
Lys Cys Thr Val	Leu Ile Gln Val Ile Asp Val Asn Asp His Ala	
	335	340 345
Pro Glu Val Thr	Met Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	
	350	355 360
Ala Pro Glu Thr	Val Val Ala Leu Phe Ser Val Ser Asp Leu Asp	
	365	370 375
Ser Gly Glu Asn	Gly Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	
	380	385 390
Pro Phe Leu Leu	Lys Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	
	395	400 405
Glu Arg Pro Leu	Asp Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	
	410	415 420
Ile Thr Val Thr	Asp Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	
	425	430 435

Asn Met Thr Val Leu Ile Ala Asp Val	Asn Asp Asn Ala Pro Ala	440	445	450
Phe Thr Gln Thr Ser Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser		455	460	465
Pro Ala Leu His Ile Arg Ser Val Ser Ala Thr Asp Arg Asp Ser		470	475	480
Gly Thr Asn Ala Gln Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp		485	490	495
Pro His Leu Pro Leu Thr Ser Leu Val Ser Ile Asn Ala Asp Asn		500	505	510
Gly His Leu Phe Ala Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln		515	520	525
Gly Phe Gln Phe Arg Val Gly Ala Ser Asp His Gly Ser Pro Ala		530	535	540
Leu Ser Ser Glu Ala Leu Val Arg Val Val Val Leu Asp Ala Asn		545	550	555
Asp Asn Ser Pro Phe Val Leu Tyr Pro Leu Gln Asn Gly Ser Ala		560	565	570
Pro Cys Thr Glu Leu Val Pro Arg Ala Ala Glu Pro Gly Tyr Leu		575	580	585
Val Thr Lys Val Val Ala Val Asp Gly Asp Ser Gly Gln Asn Ala		590	595	600
Trp Leu Ser Tyr Gln Leu Leu Lys Ala Thr Glu Leu Gly Leu Phe		605	610	615
Gly Val Trp Ala His Asn Gly Glu Val Arg Thr Ala Arg Leu Leu		620	625	630
Ser Glu Arg Asp Ala Ala Lys His Arg Leu Val Val Leu Val Lys		635	640	645
Asp Asn Gly Glu Pro Pro Arg Ser Ala Thr Ala Thr Leu His Val		650	655	660
Leu Leu Val Asp Gly Phe Ser Gln Pro Tyr Leu Pro Leu Pro Glu		665	670	675
Ala Ala Pro Thr Gln Ala Gln Ala Asp Leu Leu Thr Val Tyr Leu		680	685	690
Val Val Ala Leu Ala Ser Val Ser Ser Leu Phe Leu Phe Ser Val		695	700	705
Leu Leu Phe Val Ala Val Arg Leu Cys Arg Arg Ser Arg Ala Ala		710	715	720

Ser Val Gly Arg Cys Leu Val Pro Glu Gly Pro Leu Pro Gly His
725 730 735

Leu Val Asp Met Ser Gly Thr Arg Thr Leu Ser Gln Ser Tyr Gln
740 745 750

Tyr Glu Val Cys Leu Ala Gly Gly Ser Gly Thr Asn Glu Phe Lys
755 760 765

Phe Leu Lys Pro Ile Ile Pro Asn Phe Pro Pro Gln Cys Pro Gly
770 775 780

Lys Glu Ile Gln Gly Asn Ser Thr Phe Pro Asn Asn Phe Gly Phe
785 790 795

Asn Ile Gln

<210> 406

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 406

ctgagaacgc gcctgaaact gtg 23

<210> 407

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 407

agcgttgatc ttgacatcgg cg 22

<210> 408

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 408

ttagttgctc cattcaggag gatctacct tctctctgaa atccgcggaa 50

<210> 409

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 409

acccacgcgt cgcgccacgc gtcgcgccac gcgtccgcgc acgcgtccgc 50
 gcgtagccgt gcgcgcattg cctctcggcc tgggcaatgg tcccggtgc 100
 cggctgcagc cgcgcccgcg tcatgcggct cctcggtgg tggcaagtat 150
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200
 agtggtcgct tatggtcaga ggagcagcct gtcacccctc tccaggtggg 250
 ggctgtgtac ctgggtgagg aggagctcct gcatgacccg atggggccagg 300
 acagggcagc agaagaggcc aatgcgggtgc tggggctgga caccgaaggc 350
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500
 cacttccttg acagagaaga ggagtattac acagagccag aagtggcgga 550
 atctgacgca gccccgacag aggactocaa taacactgaa agtotgaaat 600
 ccccaaaagt gaattgtgag gagagaaaata ttacgggatt agaaaatttc 650
 actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700
 aaacggtagt gactgtactc tagtctgtt ttacaccccg tggtgccgct 750
 tttctgcag tttggccct cactttaact ctctgccccg ggcatttcca 800
 gctcttcaact ttttggcaact ggatgcactc cagcacagca gcctttctac 850
 caggtttggc accgtagctg ttctaatat tttattattt caaggagcta 900
 aaccaatggc cagatttaat cctacagatc gaacactgga aacactgaaa 950
 atcttcaatt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000
 aactcaagcc gaccaaatag gccctcttcc cagcactttg ataaaaagt 1050
 tggactcctt gctgttattt ttttattctt ttttaattag ttttattatg 1100
 tatgtataga tttaactgga gcttattcct tgggagaaat taggtataga 1150
 gacacacat atgggttgt gctgttga agaggtgg agagaggaac 1200
 ttcaatcctt cgttttagaa attagtgcta cagtttccata cttttctcc 1250
 agtgacgtgt tgaattgaaa cttaaggcag attaaaagaa tcatttggtg 1300
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350
 caataagcaa atgcaaaaat attcaatag 1379

<211> 360
<212> PRT
<213> Homo sapiens

<400> 410

Met	Val	Pro	Ala	Ala	Gly	Arg	Arg	Pro	Pro	Arg	Val	Met	Arg	Leu	
1				5					10					15	
Leu	Gly	Trp	Trp	Gln	Val	Leu	Leu	Trp	Val	Leu	Gly	Leu	Pro	Val	
				20					25					30	
Arg	Gly	Val	Glu	Val	Ala	Glu	Glu	Ser	Gly	Arg	Leu	Trp	Ser	Glu	
				35					40					45	
Glu	Gln	Pro	Ala	His	Pro	Leu	Gln	Val	Gly	Ala	Val	Tyr	Leu	Gly	
				50					55					60	
Glu	Glu	Glu	Leu	Leu	His	Asp	Pro	Met	Gly	Gln	Asp	Arg	Ala	Ala	
				65					70					75	
Glu	Glu	Ala	Asn	Ala	Val	Leu	Gly	Leu	Asp	Thr	Gln	Gly	Asp	His	
				80					85					90	
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val	
				95					100					105	
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu	
				110					115					120	
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly	
				125					130					135	
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu	
				140					145					150	
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn	
				155					160					165	
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg	
				170					175					180	
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met	
				185					190					195	
Ser	Gln	Asn	Leu	Met	Arg	Thr	Leu	Ala	Val	Asp	Gly	Ser	Asp	Cys	
				200					205					210	
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser	
				215					220					225	
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu	
				230					235					240	
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr	
				245					250					255	
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly	

260										265					270				
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 411

cacagagcca gaagtggcgg aatc 24

<210> 412

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 412

ccacatgttc ctgctcttgg cctgg 25

<210> 413

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 413

cggtagtgac tgtactctag tctgtttta caccocgtgg tgccg 45

<210> 414

<211> 1196

<212> DNA

<213> Homo sapiens

<400> 414

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agggccctgg ctgcgtgctg ctgctcttcc tcgcctcgca ctgctgectg 100
ggctcggcgc gggggtctt cctctttggc cagcccgact tctcctacaa 150
ggcgagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200
tcgaatacca gaacatgcgg ctgcccacc tgctgggcca cgagaccatg 250
aaggagggtgc tggagcaggc cggcgcttgg atcccgctgg tcatgaagca 300
gtgccacccg gacaccaaga agttcctgtg ctgcctcttc gccccctct 350
gctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400
cagggtgaagg accgctgcgc cccggtcatg tcgccttcg gcttcccctg 450
gcccagacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500
tccccctcgc tagcagcgac cactcctgc cagccaccga ggaagctcna 550
aagggtatgtg aagcctgcaa aaataaaaaat aatgatgaca agacataat 600
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agcttccccc tcccttttgc agcttgcag cccagcatt tctgagctc 1100
taaagccaca aaatgagat gctcttttgc cctccagctc agcctc 1150
aaatcttcta gaaatatcca aactaataaa ataatgaata ttttaa 1196

<210> 415

<211> 295

<212> PRT

<213> Homo sapiens

<400> 415

Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser

1	5	10	15
His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln	20	25	30
Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val	35	40	45
Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu	50	55	60
Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln	65	70	75
Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp	80	85	90
Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp	95	100	105
Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln	110	115	120
Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro	125	130	135
Trp Pro Asp Met Leu Glu Cys Asp Arg Phe Pro Gln Asp Asn Asp	140	145	150
Leu Cys Ile Pro Leu Ala Ser Ser Asp His Leu Leu Pro Ala Thr	155	160	165
Glu Glu Ala Pro Lys Val Cys Glu Ala Cys Lys Asn Lys Asn Asp	170	175	180
Asp Asp Asn Asp Ile Met Glu Thr Leu Cys Lys Asn Asp Phe Ala	185	190	195
Leu Lys Ile Lys Val Lys Glu Ile Thr Tyr Ile Asn Arg Asp Thr	200	205	210
Lys Ile Ile Leu Glu Thr Lys Ser Lys Thr Ile Tyr Lys Leu Asn	215	220	225
Gly Val Ser Glu Arg Asp Leu Tyr Tyr Ser Val Leu Trp Leu Tyr	230	235	240
Asp Ser Leu Gln Cys Thr Cys Glu Glu Met Asn Asp Ile Asn Ala	245	250	255
Pro Tyr Leu Val Met Gly Gln Lys Gln Gly Gly Glu Leu Val Ile	260	265	270
Thr Ser Val Lys Arg Trp Gln Lys Gly Gln Arg Glu Phe Lys Arg	275	280	285
Ile Ser Arg Ser Ile Arg Lys Leu Gln Cys			

<210> 416
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 416
 cctggctcgc tgetgctgct c 21

<210> 417
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 417
 cctcacaggt gcactgcaag ctgtc 25

<210> 418
 <211> 47
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 418
 ctcttctctt ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419
 <211> 1830
 <212> DNA
 <213> Homo sapiens

<400> 419
 gtggaggccg ccgacgatgg cggggccgac ggaggccgag acqddattgg 50
 ccagagcccg ggcctgttgc ggcagagggg cccacccccc ctacggcggc 100
 cgttgggtgt tctgtctcgc gatnagcctg ctcaactgct ccaacgccc 150
 gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200
 tctgtccat ggagcagatc aactggctgt cactggctca cctcgtggta 250
 tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300
 ccgtcggggc accatcctgg gtgcgtggct gaactttgac gggagtgtgc 350
 taagcatggg gccctgcctg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagcc tggatcatctt 450
ctctccagcc aagctggctg ccttgtgggtt cccagagcac cagcagacca 500
cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550
aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600
gctcgggtgc tataccatcc ctgctggcgt cgtctgectg ctgtccacca 650
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cccgtggtgg tctcactctt ccttctctct cccgtgggtg atcacgtagc 1700
tgagcgctt gtagtcacag ttgcccgcca catcgatgga ggcgaaactg 1750
aacatctggt ccacctcggg gggggggcga aagggtctct tgggggtctc 1800
gggagcgaat tacaagcgg cacctgaaaa 1830

<210> 420
 <211> 560
 <212> PRT
 <213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg	1	5	10	15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp	20	25	30	
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr	35	40	45	
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp	50	55	60	
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr	65	70	75	
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu	80	85	90	
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu	95	100	105	
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val	110	115	120	
Gly	Thr	Gln	Asn	Pro	Phe	Ala	Phe	Leu	Met	Gly	Gly	Gln	Ser	Leu	125	130	135	
Cys	Ala	Leu	Ala	Gln	Ser	Leu	Val	Ile	Phe	Ser	Pro	Ala	Lys	Leu	140	145	150	
Ala	Ala	Leu	Trp	Phe	Pro	Glu	His	Gln	Arg	Ala	Thr	Ala	Asn	Met	155	160	165	
Leu	Ala	Thr	Met	Ser	Asn	Pro	Leu	Gly	Val	Leu	Val	Ala	Asn	Val	170	175	180	
Leu	Ser	Pro	Val	Leu	Val	Lys	Lys	Gly	Gln	Asp	Ile	Pro	Leu	Met	185	190	195	
Leu	Gly	Val	Trp	Thr	Ile	Pro	Ala	Gly	Val	Val	Cys	Leu	Leu	Ser	200	205	210	
Thr	Ile	Cys	Leu	Trp	Glu	Ser	Val	Pro	Pro	Thr	Pro	Pro	Ser	Ala	215	220	225	
Gly	Ala	Ala	Ser	Ser	Thr	Ser	Glu	Lys	Phe	Leu	Asp	Gly	Leu	Lys	230	235	240	
Leu	Gln	Leu	Met	Trp	Asn	Lys	Ala	Tyr	Val	Ile	Leu	Ala	Val	Cys	245	250	255	

Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu Leu	260	265	270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser Gly	275	280	285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala Leu	290	295	300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu Ala	305	310	315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro Phe	320	325	330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala Ala	335	340	345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro Val	350	355	360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu Gly	365	370	375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly Ile	380	385	390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser Glu	395	400	405
Pro Ser Leu Ser	Thr Cys Gln Gln Gly	Glu Asp Pro Leu Asp Trp	410	415	420
Thr Val Ser Leu	Leu Leu Met Ala Gly	Leu Cys Thr Phe Phe Ser	425	430	435
Cys Ile Leu Ala	Val Phe Phe His Thr	Pro Tyr Arg Arg Leu Gln	440	445	450
Ala Glu Ser Gly	Glu Pro Pro Ser Thr	Arg Asn Ala Val Gly Gly	455	460	465
Ala Asp Ser Gly	Pro Gly Val Asp Arg	Gly Gly Ala Gly Arg Ala	470	475	480
Gly Val Leu Gly	Phe Ser Thr Ala Thr	Ile Leu Cys Ile Ala Arg	485	490	495
Gly Ala Ser Leu	Glu Asp Pro Arg Gly	Pro Gly Ser Pro His Pro	500	505	510
Ala Cys His Arg	Ala Thr Pro Arg Ala	Gln Gly Pro Ala Ala Thr	515	520	525
Asp Ala Pro Ser	Arg Pro Gly Arg Leu	Ala Gly Arg Val Gln Ala	530	535	540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser
545 550 555

Pro Trp Val Ile Thr
560

<210> 421
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 421
agctttctcag cctctctgga gcag 24

<210> 422
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 422
cgggtcaata aacctggacg cttgg 25

<210> 423
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 423
tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424
<211> 4313
<212> DNA
<213> Homo sapiens

<400> 424
gtacacata ctgttcaat tggtaggtc ctcttttagc cagatctgt cc
cctcatcttg ctgaagtggg ccaactagtt cccagtagg gggctctccc 100
tggcaantct tgatcggggt ttggacatct cagatcgtt ccaatgaaga 150
tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200
aaggttgtgc cggcagctct gggggaagga gcaagggggt gatcaagcca 250
tcaggaaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300

tctgaatcta gcccaacttgg cggtaagcat gatgcaactt ctgcaacttc 350
tgctgggggt tttggggcca ggtggctact tatttctttt aggggattgt 400
caggaggtga ccactctcac ggtgaaatac caagtgtcag aggaagtgcc 450
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<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

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Gly Tyr Leu Phe Leu Leu Gly Asp Cys Gln Glu Val Thr Thr Leu	20	25	30
Thr Val Lys Tyr Gln Val Ser Glu Glu Val Pro Ser Gly Thr Val	35	40	45
Ile Gly Lys Leu Ser Gln Glu Leu Gly Arg Glu Glu Arg Arg Arg	50	55	60
Gln Ala Gly Ala Ala Phe Gln Val Leu Gln Leu Pro Gln Ala Leu	65	70	75
Pro Ile Gln Val Asp Ser Glu Glu Gly Leu Leu Ser Thr Gly Arg	80	85	90
Arg Leu Asp Arg Glu Gln Leu Cys Arg Gln Trp Asp Pro Cys Leu	95	100	105
Val Ser Phe Asp Val Leu Ala Thr Gly Asp Leu Ala Leu Ile His	110	115	120
Val Glu Ile Gln Val Leu Asp Ile Asn Asp His Gln Pro Arg Phe	125	130	135
Pro Lys Gly Glu Gln Glu Leu Glu Ile Ser Glu Ser Ala Ser Leu	140	145	150
Arg Thr Arg Ile Pro Leu Asp Arg Ala Leu Asp Pro Asp Thr Gly	155	160	165
Pro Asn Thr Leu His Thr Tyr Thr Leu Ser Pro Ser Glu His Phe	170	175	180
Ala Leu Asp Val Ile Val Gly Pro Asp Glu Thr Lys His Ala Glu	185	190	195
Leu Ile Val Val Lys Glu Leu Asp Arg Glu Ile His Ser Phe Phe	200	205	210
Asp Leu Val Leu Thr Ala Tyr Asp Asn Gly Asn Pro Pro Lys Ser	215	220	225
Gly Thr Ser Leu Val Lys Val Asn Val Leu Asp Ser Asn Asp Asn	230	235	240
Ser Pro Ala Phe Ala Glu Ser Ser Leu His Leu Glu Ile Gln Glu	245	250	255
Asp Ala Ala Pro Gly Thr Leu Leu Ile Lys Leu Thr Ala Thr Asp	260	265	270
Pro Asp Gln Gly Pro Asn Gly Glu Val Glu Phe Phe Leu Ser Lys	275	280	285
His Met Pro Pro Glu Val Leu Asp Thr Phe Ser Ile Asp Ala Lys	290	295	300

Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys Asn
305	310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro Asn
320	325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp Val
335	340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln Pro
350	355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala Leu
365	370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val His
380	385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg Thr
395	400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp Arg
410	415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp Gln
425	430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln Ile
440	445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg Tyr
455	460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu Ile
470	475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys Val
485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala Ile
500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr
515	520	525
Gln Gln Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser
530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu
545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu
560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr
575	580	585

Gly His Leu Leu Val Pro Ile Glu Thr Pro Asn Gly Leu Gly Pro	590	595	600
Ala Gly Thr Asp Thr Pro Pro Leu Ala Thr His Ser Ser Arg Pro	605	610	615
Phe Leu Leu Thr Thr Ile Val Ala Arg Asp Ala Asp Ser Gly Ala	620	625	630
Asn Gly Glu Pro Leu Tyr Ser Ile Arg Asn Gly Asn Glu Ala His	635	640	645
Leu Phe Ile Leu Asn Pro His Thr Gly Gln Leu Phe Val Asn Val	650	655	660
Thr Asn Ala Ser Ser Leu Ile Gly Ser Glu Trp Glu Leu Glu Ile	665	670	675
Val Val Glu Asp Gln Gly Ser Pro Pro Leu Gln Thr Arg Ala Leu	680	685	690
Leu Arg Val Met Phe Val Thr Ser Val Asp His Leu Arg Asp Ser	695	700	705
Ala Arg Lys Pro Gly Ala Leu Ser Met Ser Met Leu Thr Val Ile	710	715	720
Cys Leu Ala Val Leu Leu Gly Ile Phe Gly Leu Ile Leu Ala Leu	725	730	735
Phe Met Ser Ile Cys Arg Thr Glu Lys Lys Asp Asn Arg Ala Tyr	740	745	750
Asn Cys Arg Glu Ala Glu Ser Thr Tyr Arg Gln Gln Pro Lys Arg	755	760	765
Pro Gln Lys His Ile Gln Lys Ala Asp Ile His Leu Val Pro Val	770	775	780
Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Thr Arg Thr	815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro	860	865	870

Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala	1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala	1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Thr Val	1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser	1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser	1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala	1145	1150	1155

Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr
1160 1165 1170

Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Arg Cys Leu
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<210> 426

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 426

gtaagcacat gcctccagag gtgc 24

<210> 427

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 427

gtgacgtgga tgcttgggat gttg 24

<210> 428

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 428

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<210> 429

<211> 2037

<212> DNA

<213> Homo sapiens

<400> 429

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cctgggaaaa gacagaccgt gtaaggagga ctgtgggaaa agcgtgctgt 100

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tgagtttccct catcgactcc agcatcatga ttacctccca gatactattt 200

tttggatttg ggtggctttt ctccatggga caattgttta aagactatga 250

gatacgtcag tatgtttgtac aggtgatctt ctccgtgacg ttgtcatttt 300

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<210> 430

<211> 455

<212> PRT

<213> Homo sapiens

<400> 430

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Leu	Phe	Phe	Gly	Phe	Gly	Trp	Leu	Phe	Phe	Met	Arg	Gln	Leu	Phe
			20						25					30
Lys	Asp	Tyr	Glu	Ile	Arg	Gln	Tyr	Val	Val	Gln	Val	Ile	Phe	Ser
			35						40					45
Val	Thr	Phe	Ala	Phe	Ser	Cys	Thr	Met	Phe	Glu	Leu	Ile	Ile	Phe
			50						55					60
Glu	Ile	Leu	Gly	Val	Leu	Asn	Ser	Ser	Ser	Arg	Tyr	Phe	His	Trp
			65						70					75
Lys	Met	Asn	Leu	Cys	Val	Ile	Leu	Leu	Ile	Leu	Val	Phe	Met	Val
			80						85					90
Pro	Phe	Tyr	Ile	Gly	Tyr	Phe	Ile	Val	Ser	Asn	Ile	Arg	Leu	Leu
			95						100					105
His	Lys	Gln	Arg	Leu	Leu	Phe	Ser	Cys	Leu	Leu	Trp	Leu	Thr	Phe
			110						115					120
Met	Tyr	Phe	Phe	Trp	Lys	Leu	Gln	Asp	His	Ile	Leu	Leu	Leu	Ser
			125						130					135
Pro	Lys	His	Gly	Ile	Leu	Ser	Ile	Glu	Gln	Leu	Ile	Ser	Arg	Val
			140						145					150
Gly	Val	Ile	Gly	Val	Thr	Leu	Met	Ala	Leu	Leu	Ser	Gly	Phe	Gly
			155						160					165
Ala	Val	Asn	Cys	Pro	Tyr	Thr	Tyr	Met	Ser	Tyr	Phe	Leu	Arg	Asn
			170						175					180
Val	Thr	Asp	Thr	Asp	Ile	Leu	Ala	Leu	Glu	Arg	Arg	Leu	Leu	Gln

	185	190	195
Thr Met Asp Met	Ile Ile Ser Lys Lys	Lys Arg Met Ala Met	Ala
	200	205	210
Arg Arg Thr Met	Phe Gln Lys Gly Glu	Val His Asn Lys Pro	Ser
	215	220	225
Gly Phe Trp Gly	Met Ile Lys Ser Val	Thr Thr Ser Ala Ser	Gly
	230	235	240
Ser Glu Asn Leu	Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu	Glu
	245	250	255
Glu Leu Ser Arg	Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr	Ala
	260	265	270
Thr Lys Glu Arg	Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys	Tyr
	275	280	285
Phe Asn Phe Leu	Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp	Lys
	290	295	300
Ile Phe Met Ala	Thr Ile Asn Ile Val	Phe Asp Arg Val Gly	Lys
	305	310	315
Thr Asp Pro Val	Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr	Leu
	320	325	330
Gly Ile Gln Phe	Asp Val Lys Phe Trp	Ser Gln His Ile Ser	Phe
	335	340	345
Ile Leu Val Gly	Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu	Leu
	350	355	360
Ile Thr Leu Thr	Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys	Ser
	365	370	375
Ser Asn Val Ile	Val Leu Leu Leu Ala	Gln Ile Met Gly Met	Tyr
	380	385	390
Phe Val Ser Ser	Val Leu Leu Ile Arg	Met Ser Met Pro Leu	Glu
	395	400	405
Tyr Ala Thr Ile	Ile Ile Thr Ile Ile	Gln Gln Leu Gln Ile	Asn
	410	415	420
Phe Tyr His Arg	Trp Phe Asp Val Ile	Phe Leu Val Ser Ala	Leu
	425	430	435
Ser Ser Ile Leu	Phe Leu Tyr Leu Ala	His Lys Gln Ala Pro	Glu
	440	445	450
Lys Gln Met Ala	Pro		
	455		

<211> 407
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 78, 81, 113, 157, 224, 297
<223> unknown base

<400> 431
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ttgtacnggt gatcttctcc gtgacgttg ccatttcttg caccatgttt 200
gagctcatca tctttgaaat cttaggagta ttgaatagca gctcccgtaa 250
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgac ctggttntca 300
tggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350
ataaacaac gactgctttt ttctgtctn ttatggctga cctttatgta 400
tttccag 407

<210> 432
<211> 457
<212> DNA
<213> Homo sapiens

<220>
<221> unsure
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434
<223> unknown base

<400> 432
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ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgttg 200
ccatttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250
ttgaatagca gctcccgtaa tttcactgg aaaatgaacc tgtgtgtaat 300
tctgctgac ctggttttca tggtgccttt ttacattggc tattttattg 350
tgagcaatat ccgactactg ataaacaac gactgctttt ttctgtctn 400
ttatggctga cctttatgta ttnttntgg aaantaggag atccccttcc 450

cattctc 457

<210> 433

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 433

aagtggagcc ggagccttcc 20

<210> 434

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 434

tggttgttta tgcagtagtc gg 22

<210> 435

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 435

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<210> 436

<211> 3951

<212> DNA

<213> Homo sapiens

<400> 436

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<210> 437

<211> 1141

<212> PRT

<213> Homo sapiens

<400> 437

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			20						25					30
Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
			35						40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
									55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
			65						70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly
			80						85					90
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg
			95						100					105

Val Asp Ile Asp Gln Gly Ala Asp Met Gln Lys Glu Ser Lys Glu	110	115	120
Asn Gln Trp Leu Gly Val Ser Val Arg Ser Gln Gly Pro Gly Gly	125	130	135
Lys Ile Val Thr Cys Ala His Arg Tyr Glu Ala Arg Gln Arg Val	140	145	150
Asp Gln Ile Leu Glu Thr Arg Asp Met Ile Gly Arg Cys Phe Val	155	160	165
Leu Ser Gln Asp Leu Ala Ile Arg Asp Glu Leu Asp Gly Gly Glu	170	175	180
Trp Lys Phe Cys Glu Gly Arg Pro Gln Gly His Glu Gln Phe Gly	185	190	195
Phe Cys Gln Gln Gly Thr Ala Ala Ala Phe Ser Pro Asp Ser His	200	205	210
Tyr Leu Leu Phe Gly Ala Pro Gly Thr Tyr Asn Trp Lys Gly Thr	215	220	225
Ala Arg Val Glu Leu Cys Ala Gln Gly Ser Ala Asp Leu Ala His	230	235	240
Leu Asp Asp Gly Pro Tyr Glu Ala Gly Gly Glu Lys Glu Gln Asp	245	250	255
Pro Arg Leu Ile Pro Val Pro Ala Asn Ser Tyr Phe Gly Phe Ser	260	265	270
Ile Asp Ser Gly Lys Gly Leu Val Arg Ala Glu Glu Leu Ser Phe	275	280	285
Val Ala Gly Ala Pro Arg Ala Asn His Lys Gly Ala Val Val Ile	290	295	300
Leu Arg Lys Asp Ser Ala Ser Arg Leu Val Pro Glu Val Met Leu	305	310	315
Ser Gly Glu Arg Leu Thr Ser Gly Phe Gly Tyr Ser Leu Ala Val	320	325	330
Ala Asp Leu Asn Ser Asp Gly Trp Pro Asp Leu Ile Val Gly Ala	335	340	345
Pro Tyr Phe Phe Glu Arg Gln Glu Glu Leu Gly Gly Ala Val Tyr	350	355	360
Val Tyr Leu Asn Gln Gly Gly His Trp Ala Gly Ile Ser Pro Leu	365	370	375
Arg Leu Cys Gly Ser Pro Asp Ser Met Phe Gly Ile Ser Leu Ala	380	385	390

Val Leu Gly Asp	Leu Asn Gln Asp Gly Phe Pro Asp Ile Ala Val	395	400	405
Gly Ala Pro Phe	Asp Gly Asp Gly Lys Val Phe Ile Tyr His Gly	410	415	420
Ser Ser Leu Gly	Val Val Ala Lys Pro Ser Gln Val Leu Glu Gly	425	430	435
Glu Ala Val Gly	Ile Lys Ser Phe Gly Tyr Ser Leu Ser Gly Ser	440	445	450
Leu Asp Met Asp	Gly Asn Gln Tyr Pro Asp Leu Leu Val Gly Ser	455	460	465
Leu Ala Asp Thr	Ala Val Leu Phe Arg Ala Arg Pro Ile Leu His	470	475	480
Val Ser His Glu	Val Ser Ile Ala Pro Arg Ser Ile Asp Leu Glu	485	490	495
Gln Pro Asn Cys	Ala Gly Gly His Ser Val Cys Val Asp Leu Arg	500	505	510
Val Cys Phe Ser	Tyr Ile Ala Val Pro Ser Ser Tyr Ser Pro Thr	515	520	525
Val Ala Leu Asp	Tyr Val Leu Asp Ala Asp Thr Asp Arg Arg Leu	530	535	540
Arg Gly Gln Val	Pro Arg Val Thr Phe Leu Ser Arg Asn Leu Glu	545	550	555
Glu Pro Lys His	Gln Ala Ser Gly Thr Val Trp Leu Lys His Gln	560	565	570
His Asp Arg Val	Cys Gly Asp Ala Met Phe Gln Leu Gln Glu Asn	575	580	585
Val Lys Asp Lys	Leu Arg Ala Ile Val Val Thr Leu Ser Tyr Ser	590	595	600
Leu Gln Thr Pro	Arg Leu Arg Arg Gln Ala Pro Gly Gln Gly Leu	605	610	615
Pro Pro Val Ala	Pro Ile Leu Asn Ala His Gln Pro Ser Thr Gln	620	625	630
Arg Ala Glu Ile	His Phe Leu Lys Gln Gly Cys Gly Glu Asp Lys	635	640	645
Ile Cys Gln Ser	Asn Leu Gln Leu Val His Ala Arg Phe Cys Thr	650	655	660
Arg Val Ser Asp	Thr Glu Phe Gln Pro Leu Pro Met Asp Val Asp	665	670	675

Gly Thr Thr Ala	Leu Phe Ala Leu Ser	Gly Gln Pro Val Ile Gly
680		685 690
Leu Glu Leu Met	Val Thr Asn Leu Pro	Ser Asp Pro Ala Gln Pro
695		700 705
Gln Ala Asp Gly	Asp Asp Ala His Glu	Ala Gln Leu Leu Val Met
710		715 720
Leu Pro Asp Ser	Leu His Tyr Ser Gly	Val Arg Ala Leu Asp Pro
725		730 735
Ala Glu Lys Pro	Leu Cys Leu Ser Asn	Glu Asn Ala Ser His Val
740		745 750
Glu Cys Glu Leu	Gly Asn Pro Met Lys	Arg Gly Ala Gln Val Thr
755		760 765
Phe Tyr Leu Ile	Leu Ser Thr Ser Gly	Ile Ser Ile Glu Thr Thr
770		775 780
Glu Leu Glu Val	Glu Leu Leu Leu Ala	Thr Ile Ser Glu Gln Glu
785		790 795
Leu His Pro Val	Ser Ala Arg Ala Arg	Val Phe Ile Glu Leu Pro
800		805 810
Leu Ser Ile Ala	Gly Met Ala Ile Pro	Gln Gln Leu Phe Phe Ser
815		820 825
Gly Val Val Arg	Gly Glu Arg Ala Met	Gln Ser Glu Arg Asp Val
830		835 840
Gly Ser Lys Val	Lys Tyr Glu Val Thr	Val Ser Asn Gln Gly Gln
845		850 855
Ser Leu Arg Thr	Leu Gly Ser Ala Phe	Leu Asn Ile Met Trp Pro
860		865 870
His Glu Ile Ala	Asn Gly Lys Trp Leu	Leu Tyr Pro Met Gln Val
875		880 885
Glu Leu Glu Gly	Gly Gln Gly Pro Gly	Gln Lys Gly Leu Cys Ser
890		895 900
Pro Arg Pro Asn	Ile Leu His Leu Asp	Val Asp Ser Arg Asp Arg
905		910 915
Arg Arg Arg Glu	Leu Glu Pro Pro Glu	Gln Gln Glu Pro Gly Glu
920		925 930
Arg Gln Glu Pro	Ser Met Ser Trp Trp	Pro Val Ser Ser Ala Glu
935		940 945
Lys Lys Lys Asn	Ile Thr Leu Asp Cys	Ala Arg Gly Thr Ala Asn
950		955 960

Cys Val Val Phe Ser Cys Pro Leu Tyr Ser Phe Asp Arg Ala Ala	965	970	975
Val Leu His Val Trp Gly Arg Leu Trp Asn Ser Thr Phe Leu Glu	980	985	990
Glu Tyr Ser Ala Val Lys Ser Leu Glu Val Ile Val Arg Ala Asn	995	1000	1005
Ile Thr Val Lys Ser Ser Ile Lys Asn Leu Met Leu Arg Asp Ala	1010	1015	1020
Ser Thr Val Ile Pro Val Met Val Tyr Leu Asp Pro Met Ala Val	1025	1030	1035
Val Ala Glu Gly Val Pro Trp Trp Val Ile Leu Leu Ala Val Leu	1040	1045	1050
Ala Gly Leu Leu Val Leu Ala Leu Leu Val Leu Leu Leu Trp Lys	1055	1060	1065
Met Gly Phe Phe Lys Arg Ala Lys His Pro Glu Ala Thr Val Pro	1070	1075	1080
Gln Tyr His Ala Val Lys Ile Pro Arg Glu Asp Arg Gln Gln Phe	1085	1090	1095
Lys Glu Glu Lys Thr Gly Thr Ile Leu Arg Asn Asn Trp Gly Ser	1100	1105	1110
Pro Arg Arg Glu Gly Pro Asp Ala His Pro Ile Leu Ala Ala Asp	1115	1120	1125
Gly His Pro Glu Leu Gly Pro Asp Gly His Pro Gly Pro Gly Thr	1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

120

<223> Synthetic oligonucleotide probe

<400> 438

ggc'gacacc gcagtgcctct tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 439

gctgctgggg actgcaatgt agct 24

<210> 440

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 440

catactccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441

<211> 1964

<212> DNA

<213> Homo sapiens

<400> 441

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ccgcggcggt ggtgcagcc gggggcggt cggacggcgg taattttctg 250

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<210> 442

<211> 436

<212> PPT

<213> Homo sapiens

<400> 442

Met	Leu	Lys	Val	Ser	Ala	Val	Leu	Cys	Val	Cys	Ala	Ala	Ala	Trp
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				20				25					30

Gly	Arg	Ser	Asp	Gly	Gly	Asn	Phe	Leu	Asp	Asp	Lys	Gln	Trp	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

35										40					45				
Thr	Thr	Ile	Ser	Gln	Tyr	Asp	Lys	Glu	Val	Gly	Gln	Trp	Asn	Lys					
				50					55					60					
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro					
				65				70						75					
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys					
				80				85						90					
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp					
				95				100						105					
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg					
				110				115						120					
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile					
				125				130						135					
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val					
				140				145						150					
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu					
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Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu					
				170				175						180					
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg					
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Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala					
				200				205						210					
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser					
				215				220						225					
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg					
				230				235						240					
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp					
				245				250						255					
Met	Phe	Asn	Arg	Leu	Arg	Thr	Leu	Thr	Arg	Leu	Leu	Leu	Leu	Asp	Gln				
				260				265						270					
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr					
				275				280						285					
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile					
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Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro					
				305				310						315					
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val					

				320					325					330
Lys	Lys	Leu	Leu	Gly 335	Gln	Tyr	Ile	Pro	Leu 340	Cys	Asp	Glu	Asp	Gly 345
Tyr	Tyr	Lys	Pro	Thr 350	Gln	Cys	His	Gly	Ser 355	Val	Gly	Gln	Cys	Trp 360
Cys	Val	Asp	Arg	Tyr 365	Gly	Asn	Glu	Val	Met 370	Gly	Ser	Arg	Ile	Asn 375
Gly	Val	Ala	Asp	Cys 380	Ala	Ile	Asp	Phe	Glu 385	Ile	Ser	Gly	Asp	Phe 390
Ala	Ser	Gly	Asp	Phe 395	His	Glu	Trp	Thr	Asp 400	Asp	Glu	Asp	Asp	Glu 405
Asp	Asp	Ile	Met	Asn 410	Asp	Glu	Asp	Glu	Ile 415	Glu	Asp	Asp	Asp	Glu 420
Asp	Glu	Gly	Asp	Asp 425	Asp	Asp	Gly	Gly	Asp 430	Asp	His	Asp	Val	Tyr 435

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<211> 25
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

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4400> 443
cagcaatatt cagaagcggc aaggg 25

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C210> 444
C211> 28
C212> DNA
C213> Artificial Sequence

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•213> Synthetic oligonucleotide probe

$\text{sum} = 444$
 $1 + 2 + 3 + \dots + 30 = 465$

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<210> 445
<211> 48
<212> DNA
<213> Artificial Sequence
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<220>
<223> Synthetic oligonucleotide probe

400 > 445

ggttactaca agccaacaca atgtcatggc agtgttggac agtgctgg 48

<210> 446

<211> 3617

<212> DNA

<213> Homo sapiens

<400> 446

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cagggatggg cgacaagatc tggtgcctt tccccgtgt ccttcctggc 150
gctctgcctc cgggtgtgt gctggggcg gccggcttca caccttcct 200
cgatagcgac ttcaccttta ccttcccg cggccagaag gaggcttct 250
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<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

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Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30

Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45

Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60

Glu Tyr Gln Val Leu Asp Gly Ala Gly Leu Asp Ile Asp Phe His	65	70	75
Leu Ala Ser Pro Glu Gly Lys Thr Leu Val Phe Glu Gln Arg Lys	80	85	90
Ser Asp Gly Val His Thr Val Glu Thr Glu Val Gly Asp Tyr Met	95	100	105
Phe Cys Phe Asp Asn Thr Phe Ser Thr Ile Ser Glu Lys Val Ile	110	115	120
Phe Phe Glu Leu Ile Leu Asp Asn Met Gly Glu Gln Ala Gln Glu	125	130	135
Gln Glu Asp Trp Lys Lys Tyr Ile Thr Gly Thr Asp Ile Leu Asp	140	145	150
Met Lys Leu Glu Asp Ile Leu Glu Ser Ile Asn Ser Ile Lys Ser	155	160	165
Arg Leu Ser Lys Ser Gly His Ile Gln Ile Leu Leu Arg Ala Phe	170	175	180
Glu Ala Arg Asp Arg Asn Ile Gln Glu Ser Asn Phe Asp Arg Val	185	190	195
Asn Phe Trp Ser Met Val Asn Leu Val Val Met Val Val Val Ser	200	205	210
Ala Ile Gln Val Tyr Met Leu Lys Ser Leu Phe Glu Asp Lys Arg	215	220	225

Lys Ser Arg Thr

<210> 448

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 448

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<210> 449

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 449

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<210> 450

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 450

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<210> 451

<211> 859

<212> DNA

<213> Homo sapiens

<400> 451

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aaaaaaaaa 859

<210> 452

<211> 175

<212> PRT
<213> Homo sapiens

<400> 452

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Ser	Cys	Leu	Ile	Leu	Leu	Cys	Gln	Val	Gln	Gly	Glu	Glu	Thr	Gln	
			20						25					30	
Lys	Glu	Leu	Pro	Ser	Pro	Arg	Ile	Ser	Cys	Pro	Lys	Gly	Ser	Lys	
			35						40					45	
Ala	Tyr	Gly	Ser	Pro	Cys	Tyr	Ala	Leu	Phe	Leu	Ser	Pro	Lys	Ser	
			50						55					60	
Trp	Met	Asp	Ala	Asp	Leu	Ala	Cys	Gln	Lys	Arg	Pro	Ser	Gly	Lys	
			65						70					75	
Leu	Val	Ser	Val	Leu	Ser	Gly	Ala	Glu	Gly	Ser	Phe	Val	Ser	Ser	
			80						85					90	
Leu	Val	Arg	Ser	Ile	Ser	Asn	Ser	Tyr	Ser	Tyr	Ile	Trp	Ile	Gly	
			95						100					105	
Leu	His	Asp	Pro	Thr	Gln	Gly	Ser	Glu	Pro	Asp	Gly	Asp	Gly	Trp	
			110						115					120	
Glu	Trp	Ser	Ser	Thr	Asp	Val	Met	Asn	Tyr	Phe	Ala	Trp	Glu	Lys	
			125						130					135	
Asn	Pro	Ser	Thr	Ile	Leu	Asn	Pro	Gly	His	Cys	Gly	Ser	Leu	Ser	
			140						145					150	
Arg	Ser	Thr	Gly	Phe	Leu	Lys	Trp	Lys	Asp	Tyr	Asn	Cys	Asp	Ala	
			155						160					165	
Lys	Leu	Pro	Tyr	Val	Cys	Lys	Phe	Lys	Asp						
			170						175						

<210> 453
<211> 550
<212> DNA
<213> Homo sapiens

<400> 453

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gggtctcttg ggcctgggtg ttggtgcctg cggagagctg ggcgccggcc 150
tggtctgcta cgtctgtccg gagccacag gactgtcgga ctgtgtcacc 200
atgcctacct gcaccaccaa ggaaccatg tgcaagacca cactctactc 250
ccgggagata gtgtacctct tccaggggga ctccacggtg accaagtcct 300

gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350
cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgccccg 400
tetgaacagc ctccactgcg gggccctcac gctcctccca ctcttgagcc 450
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<210> 454
<211> 125
<212> PRT
<213> Homo sapiens

<400> 454
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Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
20 25 30
Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
35 40 45
Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
50 55 60
Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
65 70 75
Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
80 85 90
Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
95 100 105
Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
110 115 120
Leu Ser Leu Arg Leu
125

<210> 1518
<211> 1518
<212> DNA
<213> Homo sapiens

<400> 455
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gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggccgctctc 200

ggcgccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250
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 aataagtacc agaccattga caactaccag ccgtaccogt gcgcagagga 400
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<210> 456

<211> 266

<212> PRT

<213> Homo sapiens

<400> 456

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Met	Val	Ala	Ala	Ala	Leu	Gly	Gly	His	Pro	Leu	Leu	Gly	Val	Ser
			20						25					30

Ala	Thr	Leu	Asn	Ser	Val	Leu	Asn	Ser	Asn	Ala	Ile	Lys	Asn	Leu
			35						40					45

Pro	Pro	Pro	Leu	Gly	Gly	Ala	Ala	Gly	His	Pro	Gly	Ser	Ala	Val
			50						55					60

Ser	Ala	Ala	Pro	Gly	Ile	Leu	Tyr	Pro	Gly	Gly	Asn	Lys	Tyr	Gln
			65						70					75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu
			80						85					90

Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp
			95						100					105

Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg
			110						115					120

Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn
			125						130					135

Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile
			140						145					150

Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu
			155						160					165

Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His
			170						175					180

Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys
			185						190					195

Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys
			200						205					210

Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg
			215						220					225

Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly
			230						235					240

Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser
			245						250					255

Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His				
			260						265					

<210> 457
<211> 638
<212> DNA
<213> Homo sapiens

<220>
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509, 556
<223> unknown base

<400> 457
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<210> 458
<211> 4040
<212> DNA
<213> Homo sapiens

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tggaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650
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 ctttcataga aattttccca ctgatagttg atttttgagg catctaatat 3600
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 ttgggttttt ctttcatagt ttgggttttt cactcctgtc cagtctattt 3700
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 aatgatactg tagttattcc agttactagt ttactgtcag aggyctgcct 3800
 ttttcagata aatattgaca taataactga agttattttt ataagaaaat 3850
 caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900
 ctcaaagaat cacaaatttg tcagtaacat gtagttgttt agttataatt 3950
 cagagtgtac agaatggtaa aaattccaat cagtcaaaaag aggtcaatga 4000
 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459
 <211> 747
 <212> PRT
 <213> Homo sapiens

<400> 459
 Met Gly Val Trp Leu Asn Lys Asp Asp Tyr Ile Arg Asp Leu Lys
 1 5 10 15
 Arg Ile Ile Leu Cys Phe Leu Ile Val Tyr Met Ala Ile Leu Val
 20 25 30
 Gly Thr Asp Gln Asp Phe Tyr Ser Leu Leu Gly Val Ser Lys Thr
 35 40 45
 Ala Ser Ser Arg Glu Ile Arg Gln Ala Phe Lys Lys Leu Ala Leu
 50 55 60
 Lys Leu His Pro Asp Lys Asn Pro Asn Asn Pro Asn Ala His Gly
 65 70 75

Asp Phe Leu Lys Ile Asn Arg Ala Tyr Glu Val Leu Lys Asp Glu	80	85	90
Asp Leu Arg Lys Lys Tyr Asp Lys Tyr Gly Glu Lys Gly Leu Glu	95	100	105
Asp Asn Gln Gly Gly Gln Tyr Glu Ser Trp Asn Tyr Tyr Arg Tyr	110	115	120
Asp Phe Gly Ile Tyr Asp Asp Asp Pro Glu Ile Ile Thr Leu Glu	125	130	135
Arg Arg Glu Phe Asp Ala Ala Val Asn Ser Gly Glu Leu Trp Phe	140	145	150
Val Asn Phe Tyr Ser Pro Gly Cys Ser His Cys His Asp Leu Ala	155	160	165
Pro Thr Trp Arg Asp Phe Ala Lys Glu Val Asp Gly Leu Leu Arg	170	175	180
Ile Gly Ala Val Asn Cys Gly Asp Asp Arg Met Leu Cys Arg Met	185	190	195
Lys Gly Val Asn Ser Tyr Pro Ser Leu Phe Ile Phe Arg Ser Gly	200	205	210
Met Ala Pro Val Lys Tyr His Gly Asp Arg Ser Lys Glu Ser Leu	215	220	225
Val Ser Phe Ala Met Gln His Val Arg Ser Thr Val Thr Glu Leu	230	235	240
Trp Thr Gly Asn Phe Val Asn Ser Ile Gln Thr Ala Phe Ala Ala	245	250	255
Gly Ile Gly Trp Leu Ile Thr Phe Cys Ser Lys Gly Gly Asp Cys	260	265	270
Leu Thr Ser Gln Thr Arg Leu Arg Leu Ser Gly Met Leu Phe Leu	275	280	285
Asn Ser Leu Asp Ala Lys Glu Ile Tyr Leu Glu Val Ile His Asn	290	295	300
Leu Pro Asp Phe Glu Leu Leu Ser Ala Asn Thr Leu Glu Asp Arg	305	310	315
Leu Ala His His Arg Trp Leu Leu Phe Phe His Phe Gly Lys Asn	320	325	330
Glu Asn Ser Asn Asp Pro Glu Leu Lys Lys Leu Lys Thr Leu Leu	335	340	345
Lys Asn Asp His Ile Gln Val Gly Arg Phe Asp Cys Ser Ser Ala	350	355	360

Pro Asp Ile Cys Ser Asn Leu Tyr Val Phe Gln Pro Ser Leu Ala	365	370	375
Val Phe Lys Gly Gln Gly Thr Lys Glu Tyr Glu Ile His His Gly	380	385	390
Lys Lys Ile Leu Tyr Asp Ile Leu Ala Phe Ala Lys Glu Ser Val	395	400	405
Asn Ser His Val Thr Thr Leu Gly Pro Gln Asn Phe Pro Ala Asn	410	415	420
Asp Lys Glu Pro Trp Leu Val Asp Phe Phe Ala Pro Trp Cys Pro	425	430	435
Pro Cys Arg Ala Leu Leu Pro Glu Leu Arg Arg Ala Ser Asn Leu	440	445	450
Leu Tyr Gly Gln Leu Lys Phe Gly Thr Leu Asp Cys Thr Val His	455	460	465
Glu Gly Leu Cys Asn Met Tyr Asn Ile Gln Ala Tyr Pro Thr Thr	470	475	480
Val Val Phe Asn Gln Ser Asn Ile His Glu Tyr Glu Gly His His	485	490	495
Ser Ala Glu Gln Ile Leu Glu Phe Ile Glu Asp Leu Met Asn Pro	500	505	510
Ser Val Val Ser Leu Thr Pro Thr Thr Phe Asn Glu Leu Val Thr	515	520	525
Gln Arg Lys His Asn Glu Val Trp Met Val Asp Phe Tyr Ser Pro	530	535	540
Trp Cys His Pro Cys Gln Val Leu Met Pro Glu Trp Lys Arg Met	545	550	555
Ala Arg Thr Leu Thr Gly Leu Ile Asn Val Gly Ser Ile Asp Cys	560	565	570
Gln Gln Tyr His Ser Phe Cys Ala Gln Glu Asn Val Gln Arg Tyr	575	580	585
Pro Glu Ile Arg Phe Phe Pro Pro Lys Ser Asn Lys Ala Tyr Gln	590	595	600
Tyr His Ser Tyr Asn Gly Trp Asn Arg Asp Ala Tyr Ser Leu Arg	605	610	615
Ile Trp Gly Leu Gly Phe Leu Pro Gln Val Ser Thr Asp Leu Thr	620	625	630
Pro Gln Thr Phe Ser Glu Lys Val Leu Gln Gly Lys Asn His Trp	635	640	645

Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	650	655	660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	665	670	675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	680	685	690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	695	700	705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	710	715	720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	725	730	735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				740	745	

<210> 460
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 460
 actcaccagc ctgttcacac tgcc 24

<210> 461
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 461
 gatcagccag ccaataccag cagg 24

<210> 462
 <211> 50
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 462
 gtggtgatga tagaatgctt tgccgaatga aaggagtc aa cagctatccc 50

<210> 463
 <211> 1818
 <212> DNA

<213> Homo sapiens

<400> 463

agacagtacc tctctcctag gactacacaa ggactgaacc agaaggaaga 50
ggacagagca aagccatgaa catcactcta gaaatecttc tgcttctgat 100
caccatcctc tactctact tggagtcgtt ggtgaagttt ttcattcttc 150
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200
catggaatag gcaggcagac tacttatgaa ttgcaaaac gacagagcat 250
attggttctg tgggatatta ataagcgcg tgtggaggaa actgcagctg 300
agtgcgagaa actaggcgctc actgcgcctg cgtatgtggt agactgcagc 350
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400
tgatgtaaca atcgtgggtga ataatgctgg gacagtatat ccagccgctc 450
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500
ctaggacatt tttggatcac aaaagcaatt ctctcctaga tgatggagag 550
aaatcatggc cacatcgta cagtggcttc agtgtgcggc cacgaagga 600
ttccttaact catcccatat tgttcacgca aatttgccgc tgttggtttt 650
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700
aacctcatgt ctctgcccag tttttgtgaa tactgggttc accaaaaatc 750
caagcacaag attatggcct gtattggaga cagatgaagt cgtagaagt 800
ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850
tatcaatata tttctgagac tacagaagtt tttctctgaa cgcgcctcag 900
cgattttaaa tcgtatgcag aatattcaat ttgaagcagt ggttggccac 950
aaaatcaaaa tgaaatgaat aaataagctc cagccagaga ctatgcctg 1000
ataatgatat gaatagtttc gaatcaatgc tgcaaaagctt tatttcacat 1050
tttttcagtc ctgataatat taaaaacatt ggtttgccac taqcaacat 1100
caaacgaaca agattaatta cctgtcttcc tgttttctca gaatatttac 1150
gtagtttttc ataggtctgt ttttctttc atgcctctta aaaacttctc 1200
tgcttacata aacatactta aaaggttttc tttaagatat tttatttttc 1250
catttaaaag tggacaaaag ctactctctt aaagttaaat aaaaagagaa 1300
cttatttaca caggggaaggt ttaagactgt tcaagtagca ttccaatctg 1350

tagccatgcc acagaatata aacaagaaca cagaatgagt gcacagctaa 1400
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450
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 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550
 aactctgaag tccacaaaaa gtggaccctc tatatttctt ccctttttat 1600
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 gaattttaag ttctagcccc atgataacct tttcttttgt aatttatgct 1700
 ttcatatata cttgggtccca gagatgttta gacaatttta ggctcaaaaa 1750
 ttaaagctaa cacaggaaaa ggaactgtac tggctattac ataagaaaca 1800
 atggacccaa gagaagaa 1818

<210> 464

<211> 300

<212> PRT

<213> Homo sapiens

<400> 464

Met	Asn	Ile	Ile	Leu	Glu	Ile	Leu	Leu	Leu	Ile	Thr	Ile	Ile	1	5	10	15	
Tyr	Ser	Tyr	Leu	Glu	Ser	Leu	Val	Lys	Phe	Phe	Ile	Pro	Gln	Arg	20	25	30	
Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	35	40	45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	50	55	60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	65	70	75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	80	85	90	
Ala	Val	Asp	Leu	Ser	Asn	Ala	Ile	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	95	100	105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	110	115	120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	125	130	135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	140	145	150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly				

155	160	165
His Ile Val Thr Val Ala Ser Val Cys Gly His Glu Gly Ile Pro		
170	175	180
Tyr Leu Ile Pro Tyr Cys Ser Ser Lys Phe Ala Ala Val Gly Phe		
185	190	195
His Arg Gly Leu Thr Ser Glu Leu Gln Ala Leu Gly Lys Thr Gly		
200	205	210
Ile Lys Thr Ser Cys Leu Cys Pro Val Phe Val Asn Thr Gly Phe		
215	220	225
Thr Lys Asn Pro Ser Thr Arg Leu Trp Pro Val Leu Glu Thr Asp		
230	235	240
Glu Val Val Arg Ser Leu Ile Asp Gly Ile Leu Thr Asn Lys Lys		
245	250	255
Met Ile Phe Val Pro Ser Tyr Ile Asn Ile Phe Leu Arg Leu Gln		
260	265	270
Lys Phe Leu Pro Glu Arg Ala Ser Ala Ile Leu Asn Arg Met Gln		
275	280	285
Asn Ile Gln Phe Glu Ala Val Val Gly His Lys Ile Lys Met Lys		
290	295	300

<210> 465
 <211> 1547
 <212> DNA
 <213> Homo sapiens

<400> 465
 cggcgccggc tgcggggcgc aggtgagggg cgcgaggtga gggcgcgag 50
 gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccg 100
 gagagggcc agcccgcccc gggcaggatg accaaggccc ggctgttcg 150
 gctgtggctg gtgtggggt cagtgttcat gattctgctg atcatcgtgt 200
 actgggacag cgcaggcgcc ggcgaatttc acttgcacac gtcccttctct 250
 aggcgcacac cggggccgcc gctgcccacg cccggggccgg acaggggacag 300
 ggagctcagc gccgaactcg atgtcgacga gtttctggac aagtttctca 350
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400
 cctgcgcggg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450
 ggcgcacgcc cggccacccc cagaccagg cccgcagcac cgggagcgga 500
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc ctccccacc 550

aaggagcgcg cattogaaga catccccaac tcggagctga gccacctgat 600
cgtggacgac cggcacgggg ccattactg ctacgtgcc aaggtggcct 650
gcaccaactg gaagcgcgtg atgacgtgc tgagcggaag cctgctgcac 700
cgcggtgcgc cctaccgca cccgctgcgc atcccgcgcg agcacgtgca 750
caacgccagc ggcacactga ccttcaacaa gttctggcgc cgctacggga 800
agctctcccg ccacctcatg aaggtcaagc tcaagaagta caccaagttc 850
ctcttcgtgc gcgacccctt cgtgcgcctg atctccgct tccgcagcaa 900
gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccacgc 950
tgcggtctga cgccaaccac accagcctgc ccgctcggc gcgcgagggc 1000
ttccgcgtg gctcaaggt gtcttcgcc aacttcaccc agtacctgct 1050
ggaccgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100
tgtaccgct ctgccaccg tgcagatcg actacgactt cgtggggaag 1150
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cgaaaaacct ctccgagact gaaagcttcc gcgttgctt ttctcgcgtg 1400
cctggaacct gacgcacgcg cactccagtt ttttatgac ctacgatitt 1450
gcaatctggg cttcttgctt actccactgc ctctatccat tgagtactgt 1500
atcgatattg ttttttaaga ttaatatatt tcaggtattt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
1				5					10					15

Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
			20					25						30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
					35				40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
			50						55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser	65	70	75
Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln	80	85	90
Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp	95	100	105
Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln	110	115	120
Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser	125	130	135
Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro	140	145	150
Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala	155	160	165
Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg	170	175	180
Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro	185	190	195
Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala	200	205	210
Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys	215	220	225
Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys	230	235	240
Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	245	250	255
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	260	265	270
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	275	280	285
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	290	295	300
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	305	310	315
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	320	325	330
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	335	340	345

Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg
				350					355					360
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser
				365					370					375
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln
				380					385					390
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr
				395					400					405
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp						
				410										

<210> 467
 <211> 1071
 <212> DNA
 <213> Homo sapiens

<400> 467
 tcggggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50
 ctttggaggt gaaagaggcc cagagtagag agagagagag accgacgtac 100
 acgggatggc tacgggaacg cgctatggcg ggaaggtggt ggtcgtgacc 150
 gggggcgggc ggcgcacggc agctgggacg gtgcgcgcct tcgtgaacag 200
 cggggcccgca gtgggttatct ggcacaagga tgagtctggg ggccggggccc 250
 tggagcagga gctccctgga gctgtcttta tctctgtga tgtgactcag 300
 gaagatgatg tgaagaccct gggttctgag accatccgcc gatttggccg 350
 cctggattgt gttgtcaaca acgctggcca ccacccaccc ccacagaggc 400
 ctgaggagac ctctgcccag ggattccgcc agctgctgga gctgaacctc 450
 ctggggacgt acaccttgac caagctcgcc ctccctacc tgcggaagag 500
 tcaagggaat gtcacaca tctccacct ggtgggggca atcgccacgg 550
 ccagggaagt tccctatgtg gccaccaagg ggcagtaac agccatgacc 600
 aaagctttgg cctgggatga aagtcctat gggtcccgag tcaactgtat 650
 ctcccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700
 tcccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750
 ggccgcatgg gccagcccgc tgaggtcggg gctccggcag tgttccctggc 800
 ctccgaagcc aacttctgca cgggcattca actgctcgtg acgggggggtg 850
 cagagctggg gtacgggtgc aagggcagtc agagcaccac cgtggacgcc 900

cccgatatcc ctctctgatt tctctcattt ctacttgggg ccccttctct 950
 aggactctcc caccctcaaac tccaacctgt atcagatgca gcccccaagc 1000
 ccttagactc taagcccagt tagcaagggtg ccgggtcacc ctgcagggtc 1050
 ccataaaaac gatttgcagc c 1071

<210> 468
 <211> 270
 <212> PRT
 <213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr
1				5					10					15
Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120
Leu	Thr	Lys	Leu	Ala	Leu	Pro	Tyr	Leu	Arg	Lys	Ser	Gln	Gly	Asn
				125					130					135
Val	Ile	Asn	Ile	Ser	Ser	Leu	Val	Gly	Ala	Ile	Gly	Gln	Ala	Gln
				140					145					150
Ala	Val	Pro	Tyr	Val	Ala	Thr	Lys	Gly	Ala	Val	Thr	Ala	Met	Thr
				155					160					165
Lys	Ala	Leu	Ala	Leu	Asp	Glu	Ser	Pro	Tyr	Gly	Val	Arg	Val	Asn
				170					175					180
Cys	Ile	Ser	Pro	Gly	Asn	Ile	Trp	Thr	Pro	Leu	Trp	Glu	Glu	Leu
				185					190					195
Ala	Ala	Leu	Met	Pro	Asp	Pro	Arg	Ala	Thr	Ile	Arg	Glu	Gly	Met
				200					205					210

Leu	Ala	Gln	Pro	Leu	Gly	Arg	Met	Gly	Gln	Pro	Ala	Glu	Val	Gly
				215					220					225
Ala	Ala	Ala	Val	Phe	Leu	Ala	Ser	Glu	Ala	Asn	Phe	Cys	Thr	Gly
				230					235					240
Ile	Glu	Leu	Leu	Val	Thr	Gly	Gly	Ala	Glu	Leu	Gly	Tyr	Gly	Cys
				245					250					255
Lys	Ala	Ser	Arg	Ser	Thr	Pro	Val	Asp	Ala	Pro	Asp	Ile	Pro	Ser
				260					265					270

<210> 469
 <211> 687
 <212> DNA
 <213> Homo sapiens

<400> 469
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 ccagcccagg agccccaaaa gaaagaggaa ggggcaaggc cggcctgggc 150
 ccttgcccc tggccctcac caggtgccac tggacctggt gtcacggatg 200
 aaacogtatg ccgcgatgga ggagtatgag aggaacatcg aggagatggt 250
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300
 acctgcagct gtggatgtcc aacaagagga gctgtctccc ctggggctac 350
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400
 gtgcctgtgt ctgggctgtg tgaacccctt caccatgcag gaggaccgca 450
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 tgcacgccac cgcacccgac agggccttgc cgcacagcgg cagtcatgga 550
 gaccatcgct gtgggctgca cctgcattct ctgaatcacc tggcccagaa 600
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 ggcatatgaa aagtaaaccac tcacttttga aagcaag 687

<210> 470
 <211> 180
 <212> PRT
 <213> Homo sapiens

<400> 470
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 1 5 10 15
 Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys
 20 25 30

Gly	Gln	Gly	Arg	Pro	Gly	Pro	Leu	Ala	Pro	Gly	Pro	His	Gln	Val	
				35					40					45	
Pro	Leu	Asp	Leu	Val	Ser	Arg	Met	Lys	Pro	Tyr	Ala	Arg	Met	Glu	
				50					55					60	
Glu	Tyr	Glu	Arg	Asn	Ile	Glu	Glu	Met	Val	Ala	Gln	Leu	Arg	Asn	
				65					70					75	
Ser	Ser	Glu	Leu	Ala	Gln	Arg	Lys	Cys	Glu	Val	Asn	Leu	Gln	Leu	
				80					85					90	
Trp	Met	Ser	Asn	Lys	Arg	Ser	Leu	Ser	Pro	Trp	Gly	Tyr	Ser	Ile	
				95					100					105	
Asn	His	Asp	Pro	Ser	Arg	Ile	Pro	Val	Asp	Leu	Pro	Glu	Ala	Arg	
				110					115					120	
Cys	Leu	Cys	Leu	Gly	Cys	Val	Asn	Pro	Phe	Thr	Met	Gln	Glu	Asp	
				125					130					135	
Arg	Ser	Met	Val	Ser	Val	Pro	Val	Phe	Ser	Gln	Val	Pro	Val	Arg	
				140					145					150	
Arg	Arg	Leu	Cys	Pro	Pro	Pro	Pro	Arg	Thr	Gly	Pro	Cys	Arg	Gln	
				155					160					165	
Arg	Ala	Val	Met	Glu	Thr	Ile	Ala	Val	Gly	Cys	Thr	Cys	Ile	Phe	
				170					175					180	

<210> 471
 <211> 2368
 <212> DNA
 <213> Homo sapiens

<400> 471
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 ctcccgccg agaagctatg ctggcgccc aaatggggg ggggggag 150
 ctcccgccg ctcccgccg ctcccgccg ctcccgccg ctcccgccg 200
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tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600
gatgtctgga atggctggtc tttttagcat ctctggcaag atatggcatt 650
ttcacaacta tttcacagtg actcttggaa ttctgtcttg gtgtttctat 700
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ctgagcgttc tgagcagaat cggagatcag aggaggtca tagagctgaa 850
cagttgcagg atgcggagga ggaaaaagat gattcaaatg aagaagaaaa 900
caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950
aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctggtgtg 1000
gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050
tgtgaccgg gaggaagtag agcctgagga ggctgaagaa ggcattctctg 1100
agcaaccctg ccagctgac acagaggtgg tggaagactc cttgaggcag 1150
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caagaataca caccaaaaaca atatgtcagc ttcccttgg cctgcagttt 1250
gtaccaaaatc ctttaattttt cctgaatgag caagcttctc ttaaaagatg 1300
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gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450
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taaccataac cctgaagct gtgaattgca aacatctcaa atgaaatgtt 1950

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 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcattctcaag 2150
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 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300
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 agggaggcta atttcttt 2368

<210> 472

<211> 349

<212> PRT

<213> Homo sapiens

<400> 472

Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala
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 20 25 30

Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser
 35 40 45

Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr
 50 55 60

Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu
 65 70 75

Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys
 80 85 90

Val Asp Val Ile Gln Glu Phe Gly Leu Ser Gly Ala Phe Phe Val
 95 100 105

Thr Thr Leu Pro Ala Phe Phe His Ala Lys Asp Gly Ile Phe Arg
 110 115 120

Arg Tyr Arg Gly Pro Gly Ile Phe Glu Asp Leu Gln Asn Tyr Ile
 125 130 135

Leu Glu Lys Lys Trp Gln Ser Val Glu Pro Leu Thr Gly Trp Lys
 140 145 150

Ser Pro Ala Ser Leu Thr Met Ser Gly Met Ala Gly Leu Phe Ser
 155 160 165

Ile Ser Gly Lys	Ile Trp His Leu His	Asn Tyr Phe Thr Val Thr	
170	175	180	
Leu Gly Ile Pro	Ala Trp Cys Ser Tyr	Val Phe Phe Val Ile Ala	
185	190	195	
Thr Leu Val Phe	Gly Leu Phe Met Gly	Leu Val Leu Val Val Ile	
200	205	210	
Ser Glu Cys Phe	Tyr Val Pro Leu Pro	Arg His Leu Ser Glu Arg	
215	220	225	
Ser Glu Gln Asn	Arg Arg Ser Glu Glu	Ala His Arg Ala Glu Gln	
230	235	240	
Leu Gln Asp Ala	Glu Glu Glu Lys Asp	Asp Ser Asn Glu Glu Glu	
245	250	255	
Asn Lys Asp Ser	Leu Val Asp Asp Glu	Glu Glu Lys Glu Asp Leu	
260	265	270	
Gly Asp Glu Asp	Glu Ala Glu Glu Glu	Glu Glu Glu Asp Asn Leu	
275	280	285	
Ala Ala Gly Val	Asp Glu Glu Arg Ser	Glu Ala Asn Asp Gln Gly	
290	295	300	
Pro Pro Gly Glu	Asp Gly Val Thr Arg	Glu Glu Val Glu Pro Glu	
305	310	315	
Glu Ala Glu Glu	Gly Ile Ser Glu Gln	Pro Cys Pro Ala Asp Thr	
320	325	330	
Glu Val Val Glu	Asp Ser Leu Arg Gln	Arg Lys Ser Gln His Ala	
335	340	345	

Asp Lys Gly Leu

<210> 473

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 473

gtccagccca tgaccgctc caac 24

<210> 474

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 474

ctctctcat ccacaccagc agcc 24

<210> 475

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 475

gtggatgctg aaattttacg ccccatgggtg tccatcctgc cagc 44

<210> 476

<211> 2478

<212> DNA

<213> Homo sapiens

<400> 476

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tcaagaacaa tggaatatca tcttgattta gaaaatttgg atgaagatgg 200
atatactcaa ttacaacttg actctcaaag caataccagg atagctgttg 250
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gggtaccatg ggggttcttt ccagcccttg tctcctaata tggattatat 400
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ctattatgg aatgaaaata tatttctca tctgtgatt tcttttattt 2250
tttccatct tccccactgg tctatttttt atttccaatg gatatttctg 2300

tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350
 agaaattgta ccaattttac taaattatgc agtttaaaat ggatgatttt 2400
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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 2478

<210> 477
 <211> 201
 <212> PRT
 <213> Homo sapiens

<400> 477
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 Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val
 20 25 30
 Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu
 35 40 45
 Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile
 50 55 60
 Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro
 65 70 75
 Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met
 80 85 90
 Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu
 95 100 105
 Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe
 110 115 120
 Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile
 125 130 135
 Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp
 140 145 150
 Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala
 155 160 165
 Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser
 170 175 180
 Val Ile Tyr Asp Gln Leu Cys Ser Val Pro Ser Tyr Ser Ile Cys
 185 190 195
 Glu Lys Lys Phe Ser Met
 200

<210> 478

<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 478
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<210> 479
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 479
araagtgtct tcccaacctg 20

<210> 480
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 480
atctctccag agccatggta cctc 24

<210> 481
<211> 51
<212> DNA
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<220>
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t g g

<210> 482
<211> 3819
<212> DNA
<213> Homo sapiens

<400> 482
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tcttggtctc tctgaacctc cactctccgg gttcaagtga ttctcatgac 150

tcajccctccc gagtagctgg gattacaggt ggtgacttcc aagagtgact 200
ccgtcggagg aaaatgactc cccagtcgct gctgcagacg aactgttcc 250
tgctgagtct gctcttctg gtccaaggtg cccacggcag gggccacagg 300
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<210> 483
 <211> 693
 <212> PRT
 <213> Homo sapiens

<400> 483
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 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn
 50 55 60
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His
 65 70 75
 Pro Ala Ser Arg Ser Phe Pro Asp Pro Arg Gly Leu Tyr His Phe
 80 85 90

Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	95	100	105
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	110	115	120
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	125	130	135
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	140	145	150
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	155	160	165
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	170	175	180
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	185	190	195
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	200	205	210
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	215	220	225
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	230	235	240
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	245	250	255
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	260	265	270
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	275	280	285
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	290	295	300
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gln	Gln	Arg	Val	Leu	Gly	Ile	305	310	315
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	320	325	330
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	335	340	345
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	350	355	360
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	365	370	375

Ser Cys Phe Cys Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val
380	385 390
Ser Ser Val Glu Val Asp Ala Val His	Lys His Tyr Leu Ser Leu
395	400 405
Leu Ser Tyr Val Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val
410	415 420
Thr Ile Ala Ala Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg
425	430 435
Arg Lys Pro Arg Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu
440	445 450
Leu Ala Val Phe Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro
455	460 465
Val Ala Leu Thr Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile
470	475 480
Phe Leu His Phe Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu
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Glu Gly Tyr Asn Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr
500	505 510
Tyr Val Pro Gly Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly
515	520 525
Phe Pro Ile Phe Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp
530	535 540
Asn Tyr Gly Pro Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly
545	550 555
Val Ile Tyr Pro Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser
560	565 570
Tyr Ile Thr Asn Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn
575	580 585
Met Ala Met Leu Ala Ser Met Val Val	Glu Thr Leu Arg Leu Arg
590	595 600
Pro His Thr Gln Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu
605	610 615
Ser Leu Val Leu Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe
620	625 630
Ala Ser Gly Thr Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile
635	640 645
Ile Thr Ser Phe Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser
650	655 660

Met Arg Leu Gln Ala Arg Gly Gly Pro Ser Pro Leu Lys Ser Asn
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Ser Asp Ser Ala Arg Leu Pro Ile Ser Ser Gly Ser Thr Ser Ser
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Ser Arg Ile

<210> 484

<211> 516

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 68, 70, 84, 147

<223> unknown base

<400> 484

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<210> 485

<211> 51

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<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 485

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<210> 486

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 486

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<210> 487

<211> 2849

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2715

<223> unknown base

<400> 487

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<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

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				20					25					30
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln
				35					40					45
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser
				50					55					60
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp
				65					70					75
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe
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Asn	Gln	Arg	Phe	Gly	Leu	Leu	Asp	Pro	Glu	Asn	Asn	Ile	Cys	Lys
				95					100					105
Tyr	Asp	Ile	Val	Gln	Val	Ala	Pro	Val	Leu	Asp	Gly	Val	Val	Val
				110					115					120
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser
				125					130					135
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe
				140					145					150
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro
				155					160					165

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<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

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Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn	35	40	45	
His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro	50	55	60	
Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn	65	70	75	
His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His	80	85	90	
Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu	95	100	105	
Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro	110	115	120	
Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp	125	130	135	
Gly	Asn	Gln	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	140	145	150	
Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys	155	160	165	
Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly	170	175	180	
Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile	185	190	195	

Glu Lys Asp Ala Phe Leu Asn Leu Thr Lys Leu Lys Val Leu Ser	200	205	210
Leu Lys Asp Asn Asn Val Thr Ala Val Pro Thr Val Leu Pro Ser	215	220	225
Thr Leu Thr Glu Leu Tyr Leu Tyr Asn Asn Met Ile Ala Lys Ile	230	235	240
Gln Glu Asp Asp Phe Asn Asn Leu Asn Gln Leu Gln Ile Leu Asp	245	250	255
Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Val Asp Leu Ser Ser Val Lys Ser Ser	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Lys Arg Phe Lys Asn Lys	470	475	480

Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp	545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu Leu His Lys Leu Glu Val	560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr Phe Gln Ser Glu Gly Ile	575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn Leu Lys Val Leu Gln Lys	590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser Ser Ser Thr Ser Arg Thr	605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu Glu Phe Arg Gly Asn His	620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp Asn Arg Tyr Leu Gln Leu	635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu Leu Asp Ile Ser Lys Asn	650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val Phe Asp Gly Met Pro Pro	665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys Asn Gly Leu Lys Ser Phe	680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys Asn Leu Glu Thr Leu Asp	695	700	705
Leu Leu His Asn Glu Leu His Thr Leu Ser Thr Thr Thr	710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile Leu Lys Asn Asn Gln Ile	725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln Asp Ala Phe Gln Leu Arg	740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile Gln Met Ile Gln Lys Thr	755	760	765

Ser Phe Pro Glu Asn Val Leu Asn Asn Leu Lys Met Leu Leu Leu	770	775	780
His His Asn Arg Phe Leu Cys Thr Cys Asp Ala Val Trp Phe Val	785	790	795
Trp Trp Val Asn His Thr Glu Val Thr Ile Pro Tyr Leu Ala Thr	800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala His Lys Gly Gln Ser Val	815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu Leu Asp Leu Thr Asn Leu	830	835	840
Ile Leu Phe Ser Leu Ser Ile Ser Val Ser Leu Phe Leu Met Val	845	850	855
Met Met Thr Ala Ser His Leu Tyr Phe Trp Asp Val Trp Tyr Ile	860	865	870
Tyr His Phe Cys Lys Ala Lys Ile Lys Gly Tyr Gln Arg Leu Ile	875	880	885
Ser Pro Asp Cys Cys Tyr Asp Ala Phe Ile Val Tyr Asp Thr Lys	890	895	900
Asp Pro Ala Val Thr Glu Trp Val Leu Ala Glu Leu Val Ala Lys	905	910	915
Leu Glu Asp Pro Arg Glu Lys His Phe Asn Leu Cys Leu Glu Glu	920	925	930
Arg Asp Trp Leu Pro Gly Gln Pro Val Leu Glu Asn Leu Ser Gln	935	940	945
Ser Ile Gln Leu Ser Lys Lys Thr Val Phe Val Met Thr Asp Lys	950	955	960
Tyr Ala Lys Thr Glu Asn Phe Lys Ile Ala Phe Tyr Leu Ser His	965	970	975
Gln Arg Leu Met Asp Glu Lys Val Asp Val Ile Ile Leu Ile Phe	980	985	990
Leu Val Lys Pro Ser Glu Lys Val Tyr Thr Val Val Val Arg Val	995	1000	1005
Arg Leu Cys Gly Ser Ser Val Leu Glu Trp Pro Thr Asn Pro Gln	1010	1015	1020
Ala His Pro Tyr Phe Trp Gln Cys Leu Lys Asn Ala Leu Ala Thr	1025	1030	1035
Asp Asn His Val Ala Tyr Ser Gln Val Phe Lys Glu Thr Val	1040	1045	

<210> 497
<211> 4199
<212> DNA
<213> Homo sapiens

<400> 497
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<210> 498

<211> 1041

<212> PRT

<213> Homo sapiens

<400> 498

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Leu	Leu	Ile	Ser	Gly	Ser	Cys	Glu	Leu	Cys	Ala	Glu	Glu	Asn	Phe
				20					25					30

Ser	Arg	Ser	Tyr	Pro	Cys	Asp	Glu	Lys	Lys	Gln	Asn	Asp	Ser	Val
				35					40					45

Ile	Ala	Glu	Cys	Ser	Asn	Arg	Arg	Leu	Gln	Glu	Val	Pro	Gln	Thr
				50					55					60

Val	Gly	Lys	Tyr	Val	Thr	Glu	Leu	Asp	Leu	Ser	Asp	Asn	Phe	Ile
				65					70					75

Thr	His	Ile	Thr	Asn	Glu	Ser	Phe	Gln	Gly	Leu	Gln	Asn	Leu	Thr
				80					85					90

Lys	Ile	Asn	Leu	Asn	His	Asn	Pro	Asn	Val	Gln	His	Gln	Asn	Gly
				95					100					105

Asn	Pro	Gly	Ile	Gln	Ser	Asn	Gly	Leu	Asn	Ile	Thr	Asp	Gly	Ala
				110					115					120

Phe	Leu	Asn	Leu	Lys	Asn	Leu	Arg	Glu	Leu	Leu	Leu	Glu	Asp	Asn
				125					130					135

Gln	Leu	Pro	Gln	Ile	Pro	Ser	Gly	Leu	Pro	Glu	Ser	Leu	Thr	Glu
				140					145					150

Leu	Ser	Leu	Ile	Gln	Asn	Asn	Ile	Tyr	Asn	Ile	Thr	Lys	Glu	Gly
				155					160					165

Ile	Ser	Arg	Leu	Ile	Asn	Leu	Lys	Asn	Leu	Tyr	Leu	Ala	Thr	Asn

Cys	Tyr	Phe	Asn	Lys	Val	Lys	Ile	Gly	Ile	Asn	Ile	Ser	Asp	Gly
				185					190					195

Val	Phe	Glu	Thr	Leu	Thr	Asn	Leu	Glu	Leu	Leu	Ser	Leu	Ser	Phe
				200					205					210

Asn	Ser	Leu	Ser	His	Val	Pro	Pro	Lys	Leu	Pro	Ser	Ser	Leu	Arg
				215					220					225

Lys	Leu	Phe	Leu	Ser	Asn	Thr	Gln	Ile	Lys	Tyr	Ile	Ser	Glu	Glu
				230					235					240

Asp Phe Lys Gly Leu Ile Asn Leu Thr Leu Leu Asp Leu Ser Gly	245	250	255
Asn Cys Pro Arg Cys Phe Asn Ala Pro Phe Pro Cys Val Pro Cys	260	265	270
Asp Gly Gly Ala Ser Ile Asn Ile Asp Arg Phe Ala Phe Gln Asn	275	280	285
Leu Thr Gln Leu Arg Tyr Leu Asn Leu Ser Ser Thr Ser Leu Arg	290	295	300
Lys Ile Asn Ala Ala Trp Phe Lys Asn Met Pro His Leu Lys Val	305	310	315
Leu Asp Leu Glu Phe Asn Tyr Leu Val Gly Glu Ile Val Ser Gly	320	325	330
Ala Phe Leu Thr Met Leu Pro Arg Leu Glu Ile Leu Asp Leu Ser	335	340	345
Phe Asn Tyr Ile Lys Gly Ser Tyr Pro Gln His Ile Asn Ile Ser	350	355	360
Arg Asn Phe Ser Lys Leu Leu Ser Leu Arg Ala Leu His Leu Arg	365	370	375
Gly Tyr Val Phe Gln Glu Leu Arg Glu Asp Asp Phe Gln Pro Leu	380	385	390
Met Gln Leu Pro Asn Leu Ser Thr Ile Asn Leu Gly Ile Asn Phe	395	400	405
Ile Lys Gln Ile Asp Phe Lys Leu Phe Gln Asn Phe Ser Asn Leu	410	415	420
Glu Ile Ile Tyr Leu Ser Glu Asn Arg Ile Ser Pro Leu Val Lys	425	430	435
Asp Thr Arg Gln Ser Tyr Ala Asn Ser Ser Ser Phe Gln Arg His	440	445	450
Ile Ala Lys Arg Arg Ser Tyr Asp Phe Ala Ile Asp Pro His Ser	455	460	465
Asn Ile Tyr His Phe Thr Arg Ser Leu Ile Lys Ile Thr Lys	470	475	480
Ala Tyr Gly Lys Ala Leu Asp Leu Ser Leu Asn Ser Ile Phe Phe	485	490	495
Ile Gly Pro Asn Gln Phe Glu Asn Leu Pro Asp Ile Ala Cys Leu	500	505	510
Asn Leu Ser Ala Asn Ser Asn Ala Gln Val Leu Ser Gly Thr Glu	515	520	525

Phe Ser Ala Ile Pro His Val Lys Tyr Leu Asp Leu Thr Asn Asn	530	535	540
Arg Leu Asp Phe Asp Asn Ala Ser Ala Leu Thr Glu Leu Ser Asp	545	550	555
Leu Glu Val Leu Asp Leu Ser Tyr Asn Ser His Tyr Phe Arg Ile	560	565	570
Ala Gly Val Thr His His Leu Glu Phe Ile Gln Asn Phe Thr Asn	575	580	585
Leu Lys Val Leu Asn Leu Ser His Asn Asn Ile Tyr Thr Leu Thr	590	595	600
Asp Lys Tyr Asn Leu Glu Ser Lys Ser Leu Val Glu Leu Val Phe	605	610	615
Ser Gly Asn Arg Leu Asp Ile Leu Trp Asn Asp Asp Asp Asn Arg	620	625	630
Tyr Ile Ser Ile Phe Lys Gly Leu Lys Asn Leu Thr Arg Leu Asp	635	640	645
Leu Ser Leu Asn Arg Leu Lys His Ile Pro Asn Glu Ala Phe Leu	650	655	660
Asn Leu Pro Ala Ser Leu Thr Glu Leu His Ile Asn Asp Asn Met	665	670	675
Leu Lys Phe Phe Asn Trp Thr Leu Leu Gln Gln Phe Pro Arg Leu	680	685	690
Glu Leu Leu Asp Leu Arg Gly Asn Lys Leu Leu Phe Leu Thr Asp	695	700	705
Ser Leu Ser Asp Phe Thr Ser Ser Leu Arg Thr Leu Leu Leu Ser	710	715	720
His Asn Arg Ile Ser His Leu Pro Ser Gly Phe Leu Ser Glu Val	725	730	735
Ser Ser Leu Lys His Leu Asp Ile Ser Ser Asn Leu Leu Lys Thr	740	745	750
Ile Asn Lys Ser Arg Leu Thr Thr Thr Thr Thr Thr Thr Thr	755	760	765
Met Leu Glu Leu His Gly Asn Pro Phe Glu Cys Thr Cys Asp Ile	770	775	780
Gly Asp Phe Arg Arg Trp Met Asp Glu His Leu Asn Val Lys Ile	785	790	795
Pro Arg Leu Val Asp Val Ile Cys Ala Ser Pro Gly Asp Gln Arg	800	805	810

Gly Lys Ser Ile Val Ser Leu Glu Leu Thr Thr Cys Val Ser Asp		
	815	825
Val Thr Ala Val Ile Leu Phe Phe Phe Thr Phe Phe Ile Thr Thr		
	830	840
Met Val Met Leu Ala Ala Leu Ala His His Leu Phe Tyr Trp Asp		
	845	855
Val Trp Phe Ile Tyr Asn Val Cys Leu Ala Lys Val Lys Gly Tyr		
	860	870
Arg Ser Leu Ser Thr Ser Gln Thr Phe Tyr Asp Ala Tyr Ile Ser		
	875	885
Tyr Asp Thr Lys Asp Ala Ser Val Thr Asp Trp Val Ile Asn Glu		
	890	900
Leu Arg Tyr His Leu Glu Glu Ser Arg Asp Lys Asn Val Leu Leu		
	905	915
Cys Leu Glu Glu Arg Asp Trp Asp Pro Gly Leu Ala Ile Ile Asp		
	920	930
Asn Leu Met Gln Ser Ile Asn Gln Ser Lys Lys Thr Val Phe Val		
	935	945
Leu Thr Lys Lys Tyr Ala Lys Ser Trp Asn Phe Lys Thr Ala Phe		
	950	960
Tyr Leu Ala Leu Gln Arg Leu Met Asp Glu Asn Met Asp Val Ile		
	965	975
Ile Phe Ile Leu Leu Glu Pro Val Leu Gln His Ser Gln Tyr Leu		
	980	990
Arg Leu Arg Gln Arg Ile Cys Lys Ser Ser Ile Leu Gln Trp Pro		
	995	1005
Asp Asn Pro Lys Ala Glu Gly Leu Phe Trp Gln Thr Leu Arg Asn		
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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 499

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<210> 500

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

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<210> 501

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<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

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<210> 505
<211> 1738
<212> DNA
<213> Homo sapiens

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(1210) 506

(1211) 273

(1212) PRT

(1213) Homo sapiens

(1400) 506

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Leu	Ser	Gly	Leu	Trp	Ala	Gly	Trp	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu

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Gly His Ser Leu Ser Ala Asp Gly Thr		Leu Cys Val Pro Lys Gly			
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Gly Pro Pro Arg Val Ala Pro Asn Pro		Thr Gly Val Asp Ser Ala			
	185		190		195
Met Lys Glu Glu Val Gln Arg Leu Gln		Ser Arg Val Asp Leu Leu			
	200		205		210
Glu Glu Lys Leu Gln Leu Val Leu Ala		Pro Leu His Ser Leu Ala			
	215		220		225
Ser Gln Ala Leu Glu His Gly Leu Pro		Asp Pro Gly Ser Leu Leu			
	230		235		240
Val His Ser Phe Gln Gln Leu Gly Arg		Ile Asp Ser Leu Ser Glu			
	245		250		255
Gln Ile Ser Phe Leu Glu Glu Gln Leu		Gly Ser Cys Ser Cys Lys			
	260		265		270

Lys Asp Ser

<210> 507
 <211> 1700
 <212> DNA
 <213> Homo sapiens

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<210> 508

<211> 213

<212> PRT

<213> Homo Sapiens

<400> 508

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25				30	
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35				40					45	

Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg	
				50					55					60	
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	
				65					70					75	
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro	
				80					85					90	
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala	
				95					100					105	
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro	
				110					115					120	
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln	
				125					130					135	
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln	
				140					145					150	
Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu	
				155					160					165	
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Pro	Lys	Gly	
				170					175					180	
Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	Pro	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					195	
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Asp	Leu	Leu	
				200					205					210	
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala	
				215					220					225	
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu	
				230					235					240	
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu	
				245					250					255	
Gln	Ile	Ser	Phe	Leu	Gln	Gln	Gln	Leu	Gly	Ser	Tyr	Ser	Cys	Lys	
				260					265					270	

Lys Asp Ser

<210> 509

<211> 1538

<212> DNA

<213> Homo sapiens

<400> 100

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cgccatgccg gaacggaggg agctgtgtcc agcctggccg ctgccgtgc 700
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gtgtgtgtgt aggtgtgtgt aggtgtgtgt aggtgtgtgt aggtgtgtgt 1450
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ctgctgctg acccccagca caataaaaat gaaacgtg 1538

<210> 510

<211> 273

<212> PRT

<213> Homo sapiens

<400> 510

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Ala	Val	Gly	Gly	Thr	Glu	His	Ala	Tyr	Arg	Pro	Gly	Arg	Arg	Val
				20					25					30
Cys	Ala	Val	Arg	Ala	His	Gly	Asp	Pro	Val	Ser	Glu	Ser	Phe	Val
				35					40					45
Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	Thr	Thr	Cys	Asp	Gly	His	Arg
				50					55					60
Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	Tyr	Arg	Thr	Ala	Tyr	Arg	Arg
				65					70					75
Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	Pro	Arg	Tyr	Ala	Cys	Cys	Pro
				80					85					90
Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	Pro	Gly	Ala	Cys	Gly	Ala	Ala
				95					100					105
Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	Gly	Gly	Ser	Cys	Val	Gln	Pro
				110					115					120
Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	Trp	Arg	Gly	Asp	Thr	Cys	Gln
				125					130					135
Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	Arg	Arg	Gly	Gly	Cys	Pro	Gln
				140					145					150
Arg	Cys	Val	Asn	Thr	Ala	Gly	Ser	Tyr	Trp	Cys	Gln	Cys	Trp	Glu
				155					160					165
Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	Thr	Leu	Cys	Val	Ile	Lys	Gly
				170					175					180
Pro	Pro	Arg	Val	Ala	Pro	Asn	Ile	Thr	Gly	Val	Asp	Ser	Ala	
				185					190					
Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	Gln	Ser	Arg	Val	Arg	Leu	Ile
				200					205					210
Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Ile	Glu	His	Gly	Leu	Ile	Asp	Ile	Gly	Ser	Leu	Ile
				230					235					240

Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu
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Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys
260 265 270

Lys Asp Ser

<210> 511

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 511

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<210> 512

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 512

ttttccactc ctgtcgggtt gg 22

<210> 513

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 513

ggtgacactt gccagtcaga tgttgatgaa tgcagtgcta ggaggg 46

<210> 514

<211> 50

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2039-2069

<223> unknown base

<400> 514

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agttgggtct ccgtgtttca ggcgggtcc ccttccctgg tctcccttct 200
cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300
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cagccccac agaacacctg aactcaaatg agatgcggga ggacugcagc 1350
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Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu	50	55	60
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu	65	70	75
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp	80	85	90
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile	95	100	105
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln	110	115	120
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile	125	130	135
Val Ivs Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro	140	145	150
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe	155	160	165
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn	170	175	180
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr	185	190	195
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser	200	205	210
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr	215	220	225
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val	230	235	240
Gly Leu Thr Tyr Ile Lys Thr Thr Thr Thr Thr Thr Thr Thr	245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val	260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asp Cys Cys Glu	275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly	290	295	300
Ile Leu Pro Leu Glu Gln Ser Gly Ser Arg Pro Pro Ser Thr Gln			

	305		310		315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu					
	320		325		330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu					
	335		340		345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala					
	350		355		360
Glu Ala Glu Lys					

<210> 516
 <211> 255
 <212> DNA
 <213> Homo sapiens

<220>
 <221> unsure
 <222> 36, 38, 88, 118, 135, 193, 213, 222
 <223> unknown base

<400> 516
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 tgaattaggt attataggga tgggtggggtt gatttttntt cctggaggct 100
 ttgtgctttg gactctcnct ttctccaca gagcncttcg accatcactg 150
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200
 tcttcactct ttntctctcc cncctcaca tetatgtctt cgccttcaac 250
 ttcct 255

<210> 517
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 517
 tttgtggtt tttgtggtt tttgtggtt tttgtggtt

<210> 518
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic oligonucleotide probe

<400> 518

gcctcgtatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

aqtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

acagcctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

ggcaaaaccc attttgggag caggaattcc aatcatgtct gtgatgggtg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gtatgtgact tcaacaaaaa atggaattta aatctccttg caaaagcttg 50

atggaataaa aatctatcag gaagagagga agcaaaaaaa caaaactga 100

caaaaaaaa gaaaaaqaag aagaaaaaaa atcatgaaa caatcagac 150

aaaaatcac aattctatct cttgggcaat cttcacgggg ctggtctgct 200

tatgtctctt ccaaaqaqtg cccgtgcga gaggagatgc caccctccc 250

aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccacccctcag 300

ctacatatt caaaacaaa tcaacaaagt gacctagcta aaccacagca 350

ccatcctcta tgetgggaat gacaagtggg gctgggatc tgggtgggtc 400

cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450
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 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600
 ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650
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 ggcacacccc gggagcagtc aggggactac gagtgcagtg cctccaatga 750
 cgtggccgcg cccgtggtac ggagagtaaa ggtcacctg aactatccac 800
 catacatttc agaagccaag ggtacaggtg tccccgtggg aaaaagggg 850
 aactgcagtc gtgaagctc agcagtcctc tcagcagaat tccagtggta 900
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 aattcaatca gtccatagag atgaa agaa agaga cctcctcctc 1600
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 aaacgtgaaa taaaaagagc aaaaaaaa 1679

<210> 523

<211> 344

<11> FRT

<213> Homo sapiens

<400> 523

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				20					25					30	
Val	Arg	Ser	Gly	Asp	Ala	Thr	Phe	Pro	Lys	Ala	Met	Asp	Asn	Val	
				35					40					45	
Thr	Val	Arg	Gln	Gly	Glu	Ser	Ala	Thr	Leu	Arg	Cys	Thr	Ile	Asp	
				50					55					60	
Asn	Arg	Val	Thr	Arg	Val	Ala	Trp	Leu	Asn	Arg	Ser	Thr	Ile	Leu	
				65					70					75	
Tyr	Ala	Gly	Asn	Asp	Lys	Trp	Cys	Leu	Asp	Pro	Arg	Val	Val	Leu	
				80					85					90	
Leu	Ser	Asn	Thr	Gln	Thr	Gln	Tyr	Ser	Ile	Glu	Ile	Gln	Asn	Val	
				95					100					105	
Asp	Val	Tyr	Asp	Glu	Gly	Pro	Tyr	Thr	Cys	Ser	Val	Gln	Thr	Asp	
				110					115					120	
Asn	His	Pro	Lys	Thr	Ser	Arg	Val	His	Leu	Ile	Val	Gln	Val	Ser	
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Pro	Lys	Ile	Val	Glu	Ile	Ser	Ser	Asp	Ile	Ser	Ile	Asn	Glu	Gly	
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Asn	Asn	Ile	Ser	Leu	Thr	Cys	Ile	Ala	Thr	Gly	Arg	Pro	Glu	Pro	
				155					160					165	
Thr	Val	Thr	Trp	Arg	His	Ile	Ser	Pro	Lys	Ala	Val	Gly	Phe	Val	
				170					175					180	
Ser	Glu	Asp	Glu	Tyr	Leu	Glu	Ile	Gln	Gly	Ile	Thr	Arg	Glu	Gln	
				185					190					195	
Ser	Gly	Asp	Tyr	Glu	Cys	Ser	Ala	Ser	Asn	Asp	Val	Ala	Ala	Pro	
				200					205					210	
Val	Val	Arg	Arg	Val	Lys	Val	Thr	Val	Asn	Lys	Pro	Pro	Tyr	Ile	
				215					220					225	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				230					235					240	
Leu	Gln	Cys	Glu	Ala	Ser	Ala	Val	Pro	Ser	Ala	Glu	Phe	Gln	Trp	
				245					250					255	
Tyr	Lys	Asp	Asp	Lys	Arg	Leu	Ile	Glu	Gly	Lys	Lys	Gly	Val	Lys	
				260					265					270	
Val	Glu	Asn	Arg	Pro	Phe	Leu	Ser	Lys	Leu	Ile	Phe	Phe	Asn	Val	
				275					280					285	

Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys
290 295 300

Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala
305 310 315

Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val
320 325 330

Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe
335 340

<210> 524

<211> 503

<212> DNA

<213> Homo sapiens

<400> 524

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tcgggcaggg ggagagcgcc acctcaggt gcactattga caaccgggtc 200
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Leu Gly Cys Leu Val Ala Leu Gly Val Gln Tyr His Arg Asp Pro
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213 Artificial Sequence

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<213> Homo Sapien

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 tgggacgttt gtcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612
 <211> 352
 <212> PRT
 <213> Homo Sapien

<400> 612
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 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn
 35 40 45
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Trp Leu
 50 55 60
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile
 65 70 75
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser
 80 85 90
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn
 95 100 105
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr

110	115	120
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125	130	135
Pro Pro Lys Ile Tyr Asp Ile Ser Asn	Asp Met Thr Val Asn Glu	
140	145	150
Gly Thr Asn Val Thr Leu Thr Cys Leu	Ala Thr Gly Lys Pro Glu	
155	160	165
Pro Ser Ile Ser Trp Arg His Ile Ser	Pro Ser Ala Lys Pro Phe	
170	175	180
Glu Asn Gly Gln Tyr Leu Asp Ile Tyr	Gly Ile Thr Arg Asp Gln	
185	190	195
Ala Gly Glu Tyr Glu Cys Ser Ala Glu	Asn Ala Val Ser Phe Pro	
200	205	210
Asp Val Arg Lys Val Lys Val Val Val	Asn Phe Ala Pro Thr Ile	
215	220	225
Gln Glu Ile Lys Ser Gly Thr Val Thr	Pro Gly Arg Ser Gly Leu	
230	235	240
Ile Arg Cys Glu Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu Trp	
245	250	255
Tyr Lys Gly Glu Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile Ile	
260	265	270
Ile Gln Asn Phe Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn Val	
275	280	285
Thr Gln Glu His Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn Lys	
290	295	300
Leu Gly Thr Thr Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser Thr	
305	310	315
Ala Gln Tyr Gly Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser Cys	
320	325	330
Trp Tyr Leu Val Ser Thr Leu Ser Ser	Phe Thr Ser Ile Phe Tyr	
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<211> 1797

<212> DNA

<213> Homo Sapien

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 35 40 45
 Leu Ala Val Val Val Ile Tyr Leu Ile Leu Leu Thr Ala Gly Ala
 50 55 60
 Gly Leu Leu Val Val Gln Val Leu Asn Leu Gln Ala Arg Leu Arg
 65 70 75
 Val Leu Glu Met Tyr Phe Leu Asn Asp Thr Leu Ala Ala Glu Asp
 80 85 90
 Ser Pro Ser Phe Ser Leu Leu Gln Ser Ala His Pro Gly Glu His
 95 100 105
 Leu Ala Gln Gly Ala Ser Arg Leu Gln Val Leu Gln Ala Gln Leu
 110 115 120
 Thr Trp Val Arg Val Ser His Glu His Leu Leu Gln Arg Val Asp
 125 130 135
 Asn Phe Thr Gln Asn Pro Gly Met Phe Arg Ile Lys Gly Gln Gln
 140 145 150
 Gly Ala Pro Gly Leu Gln Gly His Lys Gly Ala Met Gly Met Pro
 155 160 165
 Gly Ala Pro Gly Pro Pro Gly Pro Pro Ala Glu Lys Gly Ala Lys
 170 175 180
 Gly Ala Met Gly Arg Asp Gly Ala Thr Gly Pro Ser Gly Pro Gln

185					190					195				
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				200					205					210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln
				215					220					225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys
				230					235					240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro
				245					250					255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met
				260					265					270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro
				275					280					285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln
				290					295					300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val
				305					310					315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro
				320					325					330
Gly	Arg	Ala	Gly	Leu	Pro	Gly	Ser	Pro	Gly	Ser	Pro	Gly	Ala	Thr
				335					340					345
Gly	Leu	Lys	Gly	Ser	Lys	Gly	Asp	Thr	Gly	Leu	Gln	Gly	Gln	Gln
				350					355					360
Gly	Arg	Lys	Gly	Glu	Ser	Gly	Val	Pro	Gly	Pro	Ala	Gly	Val	Lys
				365					370					375
Gly	Glu	Gln	Gly	Ser	Pro	Gly	Leu	Ala	Gly	Pro	Lys	Gly	Ala	Pro
				380					385					390
Gly	Gln	Ala	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Val	Lys	Gly	Ser	Ser
				395					400					405
Gly	Gln	Gln	Gln	Val	Lys	Gln	Gln	Lys	Gly	Gln	Arg	Gly	Gln	Asn
				410					415					420
Ser	Val	Ser	Val	Arg	Ile	Val	Gly	Ser	Ser	Asn	Arg	Gly	Arg	Ala
				425					430					435
Glu	Val	Tyr	Tyr	Ser	Gly	Thr	Trp	Gly	Thr	Ile	Cys	Asp	Asp	Gln
				440					445					450
Trp	Gln	Asn	Ser	Asp	Ala	Ile	Val	Phe	Cys	Arg	Met	Leu	Gly	Tyr
				455					460					465
Ser	Lys	Gly	Arg	Ala	Leu	Tyr	Lys	Val	Gly	Ala	Gly	Thr	Gly	Gln

	470		475		480
Ile Trp Leu Asp Asn Val Gln Cys Arg Gly Thr Glu Ser Thr Leu					
	485		490		495
Trp Ser Cys Thr Lys Asn Ser Trp Gly His His Asp Cys Ser His					
	500		505		510
Glu Glu Asp Ala Gly Val Glu Cys Ser Val					
	515		520		

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 <211> 647
 <212> DNA
 <213> Homo Sapien

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 aaaaaccaa atgaaactga tggtaacttg ttccacatt gggctaactt 200
 tgctgctagg agttcaagcc atgctgcaa atcgcctctc ttgctacaga 250
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 cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350
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 aaagacgttt tctttggacc aaagatctct ttctgtatc cttgcaacaa 450
 tcaatgagaa tcttcattga ttctggagaa caccattcct gatttccac 500
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550
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 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaaa 647

<210> 616
 <211> 647
 <212> PRT
 <213> Homo Sapien

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 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg
 20 25 30
 Lys Ile Leu Lys Asp His Asn Tyr His Asn Leu Pro Glu Gly Val
 35 40 45

Ala	Asp	Leu	Thr	Gln	Ile	Asp	Val	Asn	Val	Gln	Asp	His	Phe	Trp
				50					55					60
Asp	Gly	Lys	Gly	Cys	Glu	Met	Ile	Cys	Tyr	Cys	Asn	Phe	Ser	Glu
				65					70					75
Leu	Leu	Cys	Cys	Pro	Lys	Asp	Val	Phe	Phe	Gly	Pro	Lys	Ile	Ser
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Phe	Val	Ile	Pro	Cys	Asn	Asn	Gln							
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<210> 617

<211> 2558

<212> DNA

<213> Homo Sapien

<400> 617

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<210> 618
 <211> 750
 <212> PRT
 <213> Homo Sapien

<400> 618

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Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser
 35 40 45

Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala
 50 55 60

Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His
 65 70 75

Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe
 80 85 90

Gln Leu Ala Lys Gln Ile Gln Ser Gln Trp Lys Glu Phe Gly Leu
 95 100 105

Asp Ser Val Glu Leu Ala His Tyr Asp Val Leu Leu Ser Tyr Pro
 110 115 120

Asn Lys Thr His Pro Asn Tyr Ile Ser Ile Ile Asn Glu Asp Gly
 125 130 135

Asn Glu Ile Phe Asn Thr Ser Leu Phe Gln Pro Pro Pro Pro Gly
 140 145 150

Tyr Glu Asn Val Ser Asp Ile Val Pro Pro Phe Ser Ala Phe Ser
 155 160 165

Pro Gln Gly Met Pro Gln Gly Asp Leu Val Tyr Val Asn Tyr Ala
 170 175 180

Arg Thr Glu Asp Phe Phe Lys Leu Glu Arg Asp Met Lys Ile Asn
 185 190 195

Cys Ser Gly Lys Ile Val Ile Ala Arg Tyr Gly Lys Val Phe Arg
 200 205 210

Gly Asn Lys Val	Lys Asn Ala Gln Leu	Ala Gly Ala Lys Gly Val	215	220	225
Ile Leu Tyr Ser	Asp Pro Ala Asp Tyr	Phe Ala Pro Gly Val Lys	230	235	240
Ser Tyr Pro Asp	Gly Trp Asn Leu Pro	Gly Gly Gly Val Gln Arg	245	250	255
Gly Asn Ile Leu	Asn Leu Asn Gly Ala	Gly Asp Pro Leu Thr Pro	260	265	270
Gly Tyr Pro Ala	Asn Glu Tyr Ala Tyr	Arg Arg Gly Ile Ala Glu	275	280	285
Ala Val Gly Leu	Pro Ser Ile Pro Val	His Pro Ile Gly Tyr Tyr	290	295	300
Asp Ala Gln Lys	Leu Leu Glu Lys Met	Gly Gly Ser Ala Pro Pro	305	310	315
Asp Ser Ser Trp	Arg Gly Ser Leu Lys	Val Pro Tyr Asn Val Gly	320	325	330
Pro Gly Phe Thr	Gly Asn Phe Ser Thr	His Lys Val Lys Met His	335	340	345
Ile His Ser Thr	Asn Glu Val Thr Arg	Ile Tyr Asn Val Ile Gly	350	355	360
Thr Leu Arg Gly	Ala Val Glu Pro Asp	Arg Tyr Val Ile Leu Gly	365	370	375
Gly His Arg Asp	Ser Trp Val Phe Gly	Gly Ile Asp Pro Gln Ser	380	385	390
Gly Ala Ala Val	Val His Glu Ile Val	Arg Ser Phe Gly Thr Leu	395	400	405
Lys Lys Glu Gly	Trp Arg Pro Arg Arg	Thr Ile Leu Phe Ala Ser	410	415	420
Trp Asp Ala Glu	Glu Phe Gly Leu Leu	Gly Ser Thr Glu Trp Ala	425	430	435
Glu Glu Asn Ser	Arg Leu Leu Gln Gln	Arg Gly Val Ala Tyr Ile	440	445	450
Asn Ala Asp Ser	Ser Ile Glu Gly Asn	Tyr Thr Leu Arg Val Asp	455	460	465
Cys Thr Pro Leu	Met Tyr Ser Leu Val	His Asn Leu Thr Lys Glu	470	475	480
Leu Lys Ser Trp	Asp Glu Gly Phe Glu	Gly Lys Ser Leu Tyr Glu	485	490	495

Ser Trp Thr Lys	Lys Ser Pro Ser Pro	Glu Phe Ser Gly Met	Pro
500		505	510
Arg Ile Ser Lys	Leu Gly Ser Gly Asn	Asp Phe Glu Val Phe	Phe
515		520	525
Gln Arg Leu Gly	Ile Ala Ser Gly Arg	Ala Arg Tyr Thr Lys	Asn
530		535	540
Trp Glu Thr Asn	Lys Phe Ser Gly Tyr	Pro Leu Tyr His Ser	Val
545		550	555
Tyr Glu Thr Tyr	Glu Leu Val Glu Lys	Phe Tyr Asp Pro Met	Phe
560		565	570
Lys Tyr His Leu	Thr Val Ala Gln Val	Arg Gly Gly Met Val	Phe
575		580	585
Glu Leu Ala Asn	Ser Ile Val Leu Pro	Phe Asp Cys Arg Asp	Tyr
590		595	600
Ala Val Val Leu	Arg Lys Tyr Ala Asp	Lys Ile Tyr Ser Ile	Ser
605		610	615
Met Lys His Pro	Gln Glu Met Lys Thr	Tyr Ser Val Ser Phe	Asp
620		625	630
Ser Leu Phe Ser	Ala Val Lys Asn Phe	Thr Glu Ile Ala Ser	Lys
635		640	645
Phe Ser Glu Arg	Leu Gln Asp Phe Asp	Lys Ser Asn Pro Ile	Val
650		655	660
Leu Arg Met Met	Asn Asp Gln Leu Met	Phe Leu Glu Arg Ala	Phe
665		670	675
Ile Asp Pro Leu	Gly Leu Pro Asp Arg	Pro Phe Tyr Arg His	Val
680		685	690
Ile Tyr Ala Pro	Ser Ser His Asn Lys	Tyr Ala Gly Glu Ser	Phe
695		700	705
Pro Gly Ile Tyr	Asp Ala Leu Phe Asp	Ile Glu Ser Lys Val	Asp
710		715	720
Pro Ser Lys Ala	Trp Gly Glu Val Lys	Arg Gln Ile Tyr Val	Asn
725		730	735
Ala Phe Thr Val	Gln Ala Ala Ala Glu	Thr Leu Ser Glu Val	Ala
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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 619

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<210> 620

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 620

gaacatcagc gctcccggtg attcc 25

<210> 621

<211> 46

<212> DNA

<213> Artificial Sequence

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<223> Synthetic oligonucleotide probe

<400> 621

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<210> 622

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 622

ccaaactcac ccagtgagtg tgagc 25

<210> 623

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<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 623

tggaatatca ggaatgggtg tctcc 25

<210> 624

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 624

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